

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Jacobs, Kenneth  
McCoy, John M.  
LaVallie, Edward R.  
Racie, Lisa A.  
Merberg, David  
Treacy, Maurice  
Spaulding, Vikki  
Agostino, Michael

(ii) TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES  
ENCODING THEM

(iii) NUMBER OF SEQUENCES: 219

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Genetics Institute, Inc.  
(B) STREET: 87 CambridgePark Drive  
(C) CITY: Cambridge  
(D) STATE: MA  
(E) COUNTRY: U.S.A.  
(F) ZIP: 02140

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Sprunger, Suzanne A.  
(B) REGISTRATION NUMBER: 41,323

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1800 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTTTTTTTTT	TACAGACTTC	ACAGAGAATG	CAGTTGTCTT	GACTTCAGGT	CTGTCTGTTC	60
TGTTGGCAAG	TAAATGCAGT	ACTGTTCTGA	TCCCGCTGCT	ATTAGAATGC	ATTGTGAAAC	120
GA CTGGAGTA	TGATTAAAAG	TTGTGTTCCC	CAATGCTTGG	AGTAGTGATT	GTTGAAGGAA	180
AAAATCCAGC	TGAGTGATAA	AGGCTGAGTG	TTGAGGAAAT	TTCTGCAGTT	TTAAGCAGTC	240
GTATTTGTGA	TTGAAGCTGA	GTACATTTTG	CTGGTGTATT	TTTAGGTAAA	ATGCTTTTTG	300
TTCATTTCTG	GTGGTGGGAG	GGGACTGAAG	CCTTTAGTCT	TTTCCAGATG	CAACCTTAAA	360
ATCAGTGACA	AGAAACATTC	CAAACAAGCA	ACAGTCTTCA	AGAAATTAAA	CTGGCAAGTG	420
GAAATGTTTA	AACAGTTCAG	TGATCTTTAG	TGCATTGTTT	ATGTGTGGGT	TTCTCTCTCC	480
CCTCCCTTGG	TCTTAATTCT	TACATGCAGG	AACACTCAGC	AGACACACGT	ATGCGAAGGG	540
CCAGAGAAGC	CAGACCCAGT	AAGAAAAAAT	AGCCTATTTA	CTTTAAATAA	ACCAAACATT	600
CCATTTTAAA	TGTGGGGATT	GGGAACCACT	AGTTCTTTCA	GATGGTATTC	TTCAGACTAT	660
AGAAGGAGCT	TCCAGTTGAA	TTCACCAGTG	GACAAAATGA	GGAAAACAGG	TGAACAAGCT	720
TTTTCTGTAT	TTACATACAA	AGTCAGATCA	GTTATGGGAC	AATAGTATTG	AATAGATTTC	780
AGCTTTATGC	TGGAGTAACT	GGCATGTGAG	CAAACGTGTG	TGGCGTGGGG	GTGGAGGGGT	840
GAGGTGGGCG	CTAAGCTTTT	TTTAAGATTT	TTCAGGTACC	CTTCACTAAA	GGCACCGAAG	900
GCTTAAAGTA	GGACAACCAT	GGAGCTTCCT	GTGGCAGGAG	AGACAACAAA	GCGCTATTAT	960
CCTAAGGTCA	AGAGAAGTGT	CAGCCTCACC	TGATTTTTAT	TAGTAATGAG	GA CTTGCCCTC	1020
AACTCCCTCT	TTCTGGAGTG	AAGCATCCGA	AGGAATGCTT	GAAGTACCCC	TGGGCTTCTC	1080
TTAACATTTA	AGCAAGCTGT	TTTTATAGCA	GCTCTTAATA	ATAAAGCCCA	AATCTCAAGC	1140
GGTGCTTGAA	GGGGAGGGAA	AGGGGGAAAG	CGGGCAACCA	CTTTTCCCTA	GCTTTTCCAG	1200
AAGCCTGTTA	AAAGCAAGGT	CTCCCCACAA	GCAACTTCTC	TGCCACATCG	CCACCCCGTG	1260
CCTTTTGATC	TAGCACAGAC	CCTTCACCCC	TCACCTCGAT	GCAGCCAGTA	GCTTGGATCC	1320
TTGTGGGCAT	GATCCATAAT	CGGTTTCAAG	GTAACGATGG	TGTCGAGKTC	TTTGGTGGGT	1380
TGAACTATGT	TAGAAAAGGC	CATTAATTTG	CCTGCAAATT	GTTAACAGAA	GGGTATTAAA	1440
ACCACAGCTA	AGTAGCTCTA	TTATAATACT	TATCCAGTGA	CTAAAACCAA	CTTAAACCAG	1500
TAAGTGAGAG	AATAACATGT	TCAAGAACTG	TAATGCTGGG	TGGGAACATG	TA ACTTGTAG	1560
ACTGGAGAAG	ATAGGCATTT	GAGTGGCTGA	GAGGGCTTTT	GGGTGGGAAT	GCAAAAATTC	1620

TCTGCTAAGA CTTTTTCAGG TGAACATAAC AGACTTGGCC AAGCTAGCAT CTTAGCGGAA 1680  
GCTGATCTCC AATGCTCTTC AGTAGGGTCA TGAAGGTTTT TCTTTTCCTG AGAAAACAAC 1740  
ACGTATTGTT TTCTCAGGTT TTGCTTTTTG GCCTTTTTTCT AGCTTAAAAA AAAAAAAAAA 1800

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 48 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Val Trp Val Ser Leu Ser Pro Pro Leu Val Leu Ile Leu Thr Cys Arg  
1 5 10 15  
Asn Thr Gln Gln Thr His Val Cys Glu Gly Pro Glu Lys Pro Asp Pro  
20 25 30  
Val Arg Lys Asn Ser Leu Phe Thr Leu Asn Lys Pro Asn Ile Pro Phe  
35 40 45

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1063 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AAAGTTCAT CTCTAGAACT GATTTTTATC CGTTCTGTTT TTCAGGTCTT ATCTGTGTTA 60  
GTTGTGTGTT ACTATCAGGA GGCCCCCTTT GGACCCAGTG GATACAGATT ACGACTCTTC 120  
TTTTATGGTG TATGCAATGT CATTTCTATC ACTTGTGCTT ATACATCATT TTCAATAGTT 180  
CCTCCCAGCA ATGGGACCAC TATGTGGAGA GCCACAATA CAGTCTTCAG TGCCATTTTG 240  
GCTTTTTTAC TCGTAGATGA GAAAATGGCT TATGTTGACA TGGCTACAGT TGTTTGCAGC 300  
ATCTTAGGTG TTTGTCTTGT CATGATCCCA AACATTGTTG ATGAAGACAA TTCTTTGTTA 360

AATGCCTGGA AAGAAGCCTT TGGGTACACC ATGACTGTGA TGGCTGGACT GACCACTGCT 420  
 CTCTCAATGA TAGTATACAG ATCCATCAAG GAGAAGATCA GCATGTGGAC TGCCTGTTT 480  
 ACTTTTGGTT GGACTGGGAC AATTTGGGGA ATATCTACTA TGTTTATTCT TCAAGAACCC 540  
 ATCATCCCAT TAGATGGAGA AACCTGGAGT TATCTCATTG CTATATGTGT CTGTTCTACT 600  
 GCAGCATTCT TAGGAGTTTA TTATGCCTTG GACAAATTCC ATCCAGCTTT GGTAGCACA 660  
 GTACAACATT TGGAGATTGT GGTAGCTATG GTCTTGCAGC TTCTCGTGCT GCACATATTT 720  
 CCTAGCATCT ATGATGTTTT TGGAGGGGTA ATCATTATGA TTAGTGTTTT TGTCCTTGCT 780  
 GGCTATAAAC TTTACTGGAG GAATTTAAGA AGGCAGGACT ACCAGGAAAT ATTAGACTCT 840  
 CCCATTAAAT GAATACCTGA TTATTATTGT CTCATTAATG TTCAGTTATT AATATGTATA 900  
 CTGCCATTTT AATGTTTACC TATGAATGTC TTTTGTGTTA TATAACTGAC AGAGTGCTAT 960  
 AAAATATATA ATATATACAA ATGCAGAAAA TTTATTCTAG TCTAATATAT TCAAATACAA 1020  
 ATATTAAATA TATGAAATAC GTTAAAAAAA AAAAAAAAAA AAA 1063

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Trp	Arg	Ala	Thr	Thr	Thr	Val	Phe	Ser	Ala	Ile	Leu	Ala	Phe	Leu
1				5					10				15		
Leu	Val	Asp	Glu	Lys	Met	Ala	Tyr	Val	Asp	Met	Ala	Thr	Val	Val	Cys
		20						25				30			
Ser	Ile	Leu	Gly	Val	Cys	Leu	Val	Met	Ile	Pro	Asn	Ile	Val	Asp	Glu
		35					40					45			
Asp	Asn	Ser	Leu	Leu	Asn	Ala	Trp	Lys	Glu	Ala	Phe	Gly	Tyr	Thr	Met
	50					55					60				
Thr	Val	Met	Ala	Gly	Leu	Thr	Thr	Ala	Leu	Ser	Met	Ile	Val	Tyr	Arg
65				70					75				80		
Ser	Ile	Lys	Glu	Lys	Ile	Ser	Met	Trp	Thr	Ala	Leu	Phe	Thr	Phe	Gly
			85					90					95		
Trp	Thr	Gly	Thr	Ile	Trp	Gly	Ile	Ser	Thr	Met	Phe	Ile	Leu	Gln	Glu



100	105	110
Pro Ile Ile Pro Leu Asp Gly Glu Thr Trp Ser Tyr Leu Ile Ala Ile		
115	120	125
Cys Val Cys Ser Thr Ala Ala Phe Leu Gly Val Tyr Tyr Ala Leu Asp		
130	135	140
Lys Phe His Pro Ala Leu Val Ser Thr Val Gln His Leu Glu Ile Val		
145	150	155
Val Ala Met Val Leu Gln Leu Leu Val Leu His Ile Phe Pro Ser Ile		
	165	170
Tyr Asp Val Phe Gly Gly Val Ile Ile Met Ile Ser Val Phe Val Leu		
	180	185
Ala Gly Tyr Lys Leu Tyr Trp Arg Asn Leu Arg Arg Gln Asp Tyr Gln		
	195	200
Glu Ile Leu Asp Ser Pro Ile Lys		
210	215	

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 356 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TGGCCAAAGA GGCCTAGCCG GGAGCGGGCG AGGCGGCGGC GGCAGCAGCG ATGGCAGGAA	60
TAGAGTTGGA GCGGTGCCAG CAGCAGGCGA ACGAGGTGAC GGAAATTATG CGTAACAACT	120
TCGGCAAGGT CCTGGAGCGT GGTGTGAAGC TGGCCGAAC TGCAGCAGCGT TCAGACCAAC	180
TCCTGGATAT GAGCTCAACC TTCAACAAGA CTACACAGAA CCTGGCCCAG AAGAAGTGCT	240
GGGAGAACAT CCGTTACCGG ATCTGCGTGG GGCTGGTGGT GGTTGGTGTC CTGCTCATCA	300
TCCTGATTGT GCTGCTGGTC GTCTTTCTCC CTCAGAGCAG TGACAGCAGT AGTGCC	356

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 102 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```
Met Ala Gly Ile Glu Leu Glu Arg Cys Gln Gln Gln Ala Asn Glu Val
 1           5           10           15

Thr Glu Ile Met Arg Asn Asn Phe Gly Lys Val Leu Glu Arg Gly Val
 20           25           30

Lys Leu Ala Glu Leu Gln Gln Arg Ser Asp Gln Leu Leu Asp Met Ser
 35           40           45

Ser Thr Phe Asn Lys Thr Thr Gln Asn Leu Ala Gln Lys Lys Cys Trp
 50           55           60

Glu Asn Ile Arg Tyr Arg Ile Cys Val Gly Leu Val Val Val Gly Val
 65           70           75           80

Leu Leu Ile Ile Leu Ile Val Leu Leu Val Val Phe Leu Pro Gln Ser
 85           90           95

Ser Asp Ser Ser Ser Ala
 100
```

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 92 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```
AAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 60
AAAAAAAAA AAAAAAAAAA AAAAAAAAAA AA 92
```

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1131 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGGCCTCAAC TTTGGCGTCG TGAGATTCTT GTGAGGCGTC TGCCTGGAAG CCGGCAGCAA 60  
TTTTGCTTCT TTAAAGAGAA AAAGAAGGCT AGGGACTCAG ATTCCTGGAT TCTGAGATCC 120  
AGACCAGCTC CTCCCAGACC TCTCCAGAAG AAGCCATGGG AACCCCTCGT ATCCAGCATT 180  
TGCTGATCCT CCTGGTCCTA GGAGCCTCCC TCCTGACCTC GGGCCTAGAG CTGTATTGTC 240  
AAAAGGGTCT GTCCATGACT GTGGAAGCAG ATCCAGCCAA TATGTTTAAC TGGACCACAG 300  
AGGAAGTGGA GACTTGTGAC AAAGGGGCAC TTTGCCAGGA AACCATACTA ATAATTAAAG 360  
CAGGGACTGA GACAGCCATT TTGGCCACGA AGGGCTGCAT CCCGGAAGGG GAGGAGGCCA 420  
TAACAATTGT CCAGCACTCT TCACCTCCCG GCCTGATCGT GACCTCCTAC AGTAACTACT 480  
GTGAGGATTC CTTCTGTAAT GACAAAGACA GCCTGTCTCA GTTTTGGGAG TTCAGTGAGA 540  
CCACAGCTTC CACTGTGTCA ACAACCTCC ATTGTCCAAC CTGTGTGGCT TTGGGGACCT 600  
GTTTCAGTGC TCCTTCTCTT CCCTGTCCCA ATGGTACAAC TCGATGCTAT CAAGGAAAAC 660  
TTGAGATCAC TGGAGGTGGC ATTGAGTCGT CTGTGGAGGT CAAAGGCTGT ACAGCCATGA 720  
TTGGCTGCAG GCTGATGTCT GGAATCTTAG CAGTAGGACC CATGTTTGTG AGGGAAGCGT 780  
GCCCACATCA GCTGCTCACT CAACCTCGAA AGACTGAAAA TGGGGCCACC TGTCTTCCCA 840  
TTCCTGTTTG GGGGTACAG CTA CTGCTGC CATTGCTGCT GCCATCATTT ATTCATTTTT 900  
CCTAAGAAGG CACTTCTGGG CCTGGGTCTG AGGACATCTT TTTTGA CTGG GAGCCTTCTT 960  
ACTGTTGAGG TTCAACAAGC TGAGGAGTAG ATGGGAATTT GAGGGAGAAT ACAGAGATAC 1020  
TATGAACGTA TTTGACATTT TTAATACAAT TTCTGCTATA ATTTTGTAT GCAGTAGGCG 1080  
TTACTAATAA ACATTTCTGC TGTGAAAAAA AAAAAAAAAA AAAAAAAAAA A 1131

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Gly Thr Pro Arg Ile Gln His Leu Leu Ile Leu Leu Val Leu Gly  
1 5 10 15



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GCTCCGGGCC	GGCTGCGGAG	CGACTCCCCG	CCGCCAAGTG	GGCGGCGTGG	CTGTCTGGGAA	60
AGAAGGGCTG	GGGCCTGCCG	TTCTTCCTCC	CGAGTATCCC	CTCCAGCTGG	ACGACCCAC	120
GCTGCAGCAC	GGGCTTCCGG	CTTCTCTCCT	CAGTGGCCAA	TTCGAGGGCA	CAGCGGGCTC	180
CGGAGGCGCG	GCGGCAAGCC	TATCCCGCCT	CCCAACCACA	GCCTCCAGCA	CCCAGAGAA	240
CGGCCGCCCA	CAGCACACGT	TCTCCGACA	GGAGGGCGAA	GGCCCAAGAC	CTGGAGAGAT	300
GGTCAGCTCT	CAAAAAGGC	ACAAACAATT	GAAGGATGGA	TACCATGGCA	TATGTTAAAA	360
GCGTGTTGAA	AGGAAAATAA	GAAAGCCAGG	AATCTCAGGA	TGAATCAGTC	TAGATCGAGA	420
TCAGATGGTG	GCAGTGAAGA	AACCTTACCT	CAAGACCATA	ATCATCATGA	AAATGAGAGA	480
AGATGGCAGC	AAGAGCGTCT	CCACAGAGAA	GAGGCCTATT	ATCAGTTTAT	TAATGAACTC	540
AATGATGAAG	ATTATCGGCT	TATGAGAGAC	CATAATCTTT	TAGGCACCCC	TGGAGAAATA	600
ACATCAGAAG	AACTGCAACA	GCGGTTAGAT	GGCGTCAAGG	AACAAC TAGC	ATCTCAGCCT	660
GACTTGAGAG	ATGGAACGAA	TTACAGAGAC	TCAGAAGTCC	CTAGAGAAAG	TTCACATGAA	720
GATTCTCTTC	TAGAATGGTT	GAACACCTTT	CGGCGCACAG	GAAATGCAAC	TCGAAGTGGA	780
CAAAATGGGA	ACCAAAC TTG	GAGAGCTGTG	AGTCGAACAA	ACCCGAACAA	TGGAGAGTTT	840
CGGTTTAGTT	TGGAAATCCA	CGTAAATCAT	GAAAATAGAG	GATTTGAAAT	TCATGGAGAA	900
GATTATACAG	ACATTCCACT	TTCAGATAGT	AACAGAGATC	ATACTGCAAA	TAGGCAACAA	960
AGGTCAACTA	GTCCTGTGGC	TAGGCGAACA	AGAAGCCAAA	CCTCAGTGAA	TTTCAATGGT	1020
AGTAGTTCCA	ACATTCCAAG	GA CTAGGCTT	GCTTCAAGGG	GGCAAAATCC	AGCTGAAGGA	1080
TCTTTCTCAA	CATTGGGAAG	GTTAAGAAAT	GGAATTGGGG	GAGCAGCTGG	CATTCTCTCGA	1140
GCTAACGCTT	CACGCACTAA	TTTCAGTAGT	CACACAAACC	AATCAGGTGG	TAGTGAATCTC	1200
AGGCAAAGGG	AGGGGCAACG	GTTTGGAGCA	GCACATGTTT	GGGAAAATGG	GGCTAGAAGT	1260
AATGTTACAG	TGAGGAATAC	AAACCAAAGA	TTAGAGCCAA	TAAGATTACG	ATCTACTTCC	1320
AATAGTCGAA	GCCGTTCAAC	AATTCAGAGA	CAGAGTGGCA	CTGTTTATCA	TAATTCCCAA	1380
AGGGAAAGTA	GACCAGTACA	GCAAACCACT	AGAAGATCTG	TTAGGAGGAG	AGGTAGAACT	1440
CGAGTCTTTT	TAGAGCAAGA	TAGAGAACGA	GAACGCAGAG	GTACTGCATA	TACCCCATTC	1500
TCTAATTCAA	GGCTTG TGTC	AAGAATAACA	GTAGAAGAAG	GAGAAGAATC	CAGCAGATCC	1560
TCAACTGCTG	TACGACGACA	TCCAACAATC	ACACTGGACC	TTCAAGTGAG	AAGGATCCGT	1620

CCTGGAGAAA	ATAGAGATCG	GGATAGTATT	GCAAATAGAA	CTCGATCCAG	AGTAGGGCTA	1680
GCAGAAAATA	CAGTCACTAT	TGAAAGCAAT	AGTGGGGGCT	TTCGCCGAAC	CATTTCTCGT	1740
TTAGAGCGGT	CAGGTATTCG	AACCTATGTT	AGTACCATAA	CAGTTCCCCT	TCGTAGGATT	1800
TCTGAGAATG	AGCTTGTTGA	GCCATCATCA	GTGGCTCTTC	GGTCAATTTT	AAGGCAGATC	1860
ATGACTGGGT	TTGGAGAACT	GAGTTCTCTA	ATGGAGGCCG	ATTCTGAGTC	AGAACTTCAA	1920
AGAAATGGCC	AGCATTTACC	AGACATGCAC	TCAGAACTGA	GTAACCTAGG	TACAGATAAC	1980
AACAGGAGCC	AGCACAGGGA	AGGTTCCCTCT	CAAGACAGGC	AGGCCCAAGG	AGACAGCACT	2040
GAAATGCATG	GTGAAAACGA	GACCACCCAG	CCTCATACTC	GAAACAGTGA	CAGTAGGGGT	2100
GGCAGGCAGT	TGCGAAATCC	AAACAATTTA	GTTGAAACTG	GAACACTACC	CATTCTTCGC	2160
CTTGCTCACT	TTTTTTTACT	AAATGAAAGT	GATGATGATG	ATCGAATACG	TGGTTTAACC	2220
AAAGAGCAGA	TTGACAATCT	TTCCACCAGG	CACTATGAGC	ATAACAGTAT	TGATAGTGAA	2280
CTAGGTAAAA	TCTGTAGTGT	TTGTATTAGT	GACTATGTAA	CTGGAAACAA	GCTCAGGCAA	2340
TTACCTTGCA	TGCATGAATT	TCACATTCAT	TGTATTGACC	GATGGCTCTC	AGAGAATTGC	2400
ACTTGTC CGA	TCTGTCGGCA	GCCTGTTTTA	GGGTCTAACA	TAGCAAACAA	TGGGTAAGGT	2460
GATGGGATCT	ACTCAAATAC	TGTTTTTTAG	TAGAACTGAA	TGTTCAAGCA	TTGTTTTGCT	2520
GAGTTATTTG	TGATTAGCTA	ACCAGGATGA	AAAATAACAG	ATTATATATA	GTTTGAAC TA	2580
TTTTTCGTGT	GCTTTTTTAA	ACTTGTTAAA	AAGAAATTTA	TATAAAATTT	AAAATACAAA	2640
TGTAAATTA	TCCAGAAATA	CAGAATAGTT	AATATTGCTA	GAACCAAATA	ACCTCTAAAA	2700
TGTTTTTATT	TTGGTAATTT	TGTCATGCTA	AGCACTTTTG	TATCTGCACA	ATTCAGTAGG	2760
TTAAGAATCA	ATCTTCTTTT	TCTTAATAGT	ACAGCAGACT	TTAGCTTCAA	GTTTCATAGG	2820
CTTAGTACTT	ATATCTAGAC	ATTTGTGTCT	AAATAAGCTT	TTCATTAACT	TTTTATTTTA	2880
AGGACAGTAT	CTTTTCATGA	AAGAGTATTT	GGCTGAATGT	TTGCTATATA	TATGTTACTT	2940
GAAATGTTAA	ATTTAATATG	CAGCATACCA	TAGGTGTATA	TATAGGTATA	TAATTTTAAG	3000
GTTAAAATAT	TCAGTCTAAC	AAGTTTG GTT	CTTATTTAAG	CTTTTGGGCT	AATACTGCAT	3060
ATGGCACAAAT	GTTTAATATT	GGCAAGTTCA	TCTCAGAGAA	AGGGGATTCA	GATATAATTT	3120
TAAAGTAGAG	ATAATTTACT	GAAGCGTCTC	TGACAATCTA	ACTTATTAGA	CAGCAAGCAA	3180
TATATAATAC	TGAAAAAGTA	TTCAGAAATG	GAAAATTTAC	ATCATATAGG	TTATTTAACT	3240
TGTGTT CAGC	CTTTTTGTAA	CTTTTTTGAA	AGTGCAAACA	ATTCCTTGGA	TTATTAAATA	3300

AGGTATACAG TATGCATGGT TTCTCAAATT TAGCTTTAAA ATCTAAAAGT CTATAAAGAA 3360  
 TCAGATGCAT AGGCAATATG TTAAGTTCAC TTGGAGGCTA AAAATCTCCA GTGAAAACAA 3420  
 AACGAAAACC TTTAAGAGAA TGTAAGATTT ATATAAACAC AAAGTATGCA TTGAAGATCT 3480  
 GTTTCTACCA ATAAACATTA AAACAAAAAA AAAAAAAAAA AAAAAAA 3527

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 685 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met	Asn	Gln	Ser	Arg	Ser	Arg	Ser	Asp	Gly	Gly	Ser	Glu	Glu	Thr	Leu	1	5	10	15
Pro	Gln	Asp	His	Asn	His	His	Glu	Asn	Glu	Arg	Arg	Trp	Gln	Gln	Glu	20	25	30	
Arg	Leu	His	Arg	Glu	Glu	Ala	Tyr	Tyr	Gln	Phe	Ile	Asn	Glu	Leu	Asn	35	40	45	
Asp	Glu	Asp	Tyr	Arg	Leu	Met	Arg	Asp	His	Asn	Leu	Leu	Gly	Thr	Pro	50	55	60	
Gly	Glu	Ile	Thr	Ser	Glu	Glu	Leu	Gln	Gln	Arg	Leu	Asp	Gly	Val	Lys	65	70	75	80
Glu	Gln	Leu	Ala	Ser	Gln	Pro	Asp	Leu	Arg	Asp	Gly	Thr	Asn	Tyr	Arg	85	90	95	
Asp	Ser	Glu	Val	Pro	Arg	Glu	Ser	Ser	His	Glu	Asp	Ser	Leu	Leu	Glu	100	105	110	
Trp	Leu	Asn	Thr	Phe	Arg	Arg	Thr	Gly	Asn	Ala	Thr	Arg	Ser	Gly	Gln	115	120	125	
Asn	Gly	Asn	Gln	Thr	Trp	Arg	Ala	Val	Ser	Arg	Thr	Asn	Pro	Asn	Asn	130	135	140	
Gly	Glu	Phe	Arg	Phe	Ser	Leu	Glu	Ile	His	Val	Asn	His	Glu	Asn	Arg	145	150	155	160
Gly	Phe	Glu	Ile	His	Gly	Glu	Asp	Tyr	Thr	Asp	Ile	Pro	Leu	Ser	Asp	165	170	175	
Ser	Asn	Arg	Asp	His	Thr	Ala	Asn	Arg	Gln	Gln	Arg	Ser	Thr	Ser	Pro	180	185	190	

Val Ala Arg Arg Thr Arg Ser Gln Thr Ser Val Asn Phe Asn Gly Ser  
 195 200 205  
 Ser Ser Asn Ile Pro Arg Thr Arg Leu Ala Ser Arg Gly Gln Asn Pro  
 210 215 220  
 Ala Glu Gly Ser Phe Ser Thr Leu Gly Arg Leu Arg Asn Gly Ile Gly  
 225 230 235 240  
 Gly Ala Ala Gly Ile Pro Arg Ala Asn Ala Ser Arg Thr Asn Phe Ser  
 245 250 255  
 Ser His Thr Asn Gln Ser Gly Gly Ser Glu Leu Arg Gln Arg Glu Gly  
 260 265 270  
 Gln Arg Phe Gly Ala Ala His Val Trp Glu Asn Gly Ala Arg Ser Asn  
 275 280 285  
 Val Thr Val Arg Asn Thr Asn Gln Arg Leu Glu Pro Ile Arg Leu Arg  
 290 295 300  
 Ser Thr Ser Asn Ser Arg Ser Arg Ser Pro Ile Gln Arg Gln Ser Gly  
 305 310 315 320  
 Thr Val Tyr His Asn Ser Gln Arg Glu Ser Arg Pro Val Gln Gln Thr  
 325 330 335  
 Thr Arg Arg Ser Val Arg Arg Arg Gly Arg Thr Arg Val Phe Leu Glu  
 340 345 350  
 Gln Asp Arg Glu Arg Glu Arg Arg Gly Thr Ala Tyr Thr Pro Phe Ser  
 355 360 365  
 Asn Ser Arg Leu Val Ser Arg Ile Thr Val Glu Glu Gly Glu Glu Ser  
 370 375 380  
 Ser Arg Ser Ser Thr Ala Val Arg Arg His Pro Thr Ile Thr Leu Asp  
 385 390 395 400  
 Leu Gln Val Arg Arg Ile Arg Pro Gly Glu Asn Arg Asp Arg Asp Ser  
 405 410 415  
 Ile Ala Asn Arg Thr Arg Ser Arg Val Gly Leu Ala Glu Asn Thr Val  
 420 425 430  
 Thr Ile Glu Ser Asn Ser Gly Gly Phe Arg Arg Thr Ile Ser Arg Leu  
 435 440 445  
 Glu Arg Ser Gly Ile Arg Thr Tyr Val Ser Thr Ile Thr Val Pro Leu  
 450 455 460  
 Arg Arg Ile Ser Glu Asn Glu Leu Val Glu Pro Ser Ser Val Ala Leu  
 465 470 475 480  
 Arg Ser Ile Leu Arg Gln Ile Met Thr Gly Phe Gly Glu Leu Ser Ser  
 485 490 495



Leu Met Glu Ala Asp Ser Glu Ser Glu Leu Gln Arg Asn Gly Gln His  
 500 505 510  
 Leu Pro Asp Met His Ser Glu Leu Ser Asn Leu Gly Thr Asp Asn Asn  
 515 520 525  
 Arg Ser Gln His Arg Glu Gly Ser Ser Gln Asp Arg Gln Ala Gln Gly  
 530 535 540  
 Asp Ser Thr Glu Met His Gly Glu Asn Glu Thr Thr Gln Pro His Thr  
 545 550 555 560  
 Arg Asn Ser Asp Ser Arg Gly Gly Arg Gln Leu Arg Asn Pro Asn Asn  
 565 570 575  
 Leu Val Glu Thr Gly Thr Leu Pro Ile Leu Arg Leu Ala His Phe Phe  
 580 585 590  
 Leu Leu Asn Glu Ser Asp Asp Asp Arg Ile Arg Gly Leu Thr Lys  
 595 600 605  
 Glu Gln Ile Asp Asn Leu Ser Thr Arg His Tyr Glu His Asn Ser Ile  
 610 615 620  
 Asp Ser Glu Leu Gly Lys Ile Cys Ser Val Cys Ile Ser Asp Tyr Val  
 625 630 635 640  
 Thr Gly Asn Lys Leu Arg Gln Leu Pro Cys Met His Glu Phe His Ile  
 645 650 655  
 His Cys Ile Asp Arg Trp Leu Ser Glu Asn Cys Thr Cys Pro Ile Cys  
 660 665 670  
 Arg Gln Pro Val Leu Gly Ser Asn Ile Ala Asn Asn Gly  
 675 680 685

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CAGCCTGGGC TCCGCGCAGC CCACCGATCT GGGCGCCCAC AAGCGGCCGG CATCCGTGTC 60  
 GAGCAGCGCT GCCGTGGAGC ACGAGCAGCG TGAGGCGGCA GCCAAGGAGA AACAACCGCC 120  
 GCCGCCTGCG CACCGGGGCC CGGCCGACAG CCTGTCCACC GCGGCCGGGG CCGCCGAGCT 180

GAGCGCGGAA GGTGCGGGCA AGAGCCGCGG GTCTGGAGAG CAGGACTGGG TCAACAGGCC	240
CAAGACCGTG CGCGACACGC TGCTGGCGCT GCACCAGCAC GGCCACTCGG GGCCCTTCGA	300
GAGCAAGTTT AAGAAGGAGC CGGCCCTGAC TGCAGGCAGG TTGTTGGGTT TCGAGGCCAA	360
CGGGGCCAAC GGGTCTAAAG CAGTTGCAAG AACAGCAAGG AAAAGGAAGC CCTCTCCAGA	420
ACCAGAAGGT GAAGTCGGGC CCCCTAAGAT CAACGGAGAG GCCCAGCCGT GGCTGTCCAC	480
ATCCACAGAG GGGCTCAAGA TCCCCATGAC TCCTACATCC TCTTTTGTGT CTCCGCCACC	540
ACCCACTGCC TCACCTCATT CCAACCGGAC CACACGCGCT GAAGCGGCCC AGAATGGCCA	600
GTCCCCCATG GCAGCCCTGA TCTTAGTAGC AGACAATGCA GGGGGCAGTC ATGCCTCAAA	660
AGATGCCAAC CAGGTTCACT CCACTACCAG GAGGAATAGC AACAGTCCGC CCTCTCCGTC	720
CTCTATGAAC CAAAGAAGGC TGGGCCCCAG AGAGGTGGGG GGCCAGGGAG CAGGCAACAC	780
AGGAGGACTG GAGCCAGTGC ACCCTGCCAG CCTCCCGGAC TCCTCTCTGG CAACCAGTGC	840
CCCGCTGTGC TGCACCCTCT GCCACGAGCG GCTGGAGGAC ACCCATTTTG TGCAGTGCCC	900
GTCCGTCCCT TCGCACAAGT TCTGCTTCCC TTGCTCCAGA CAAAGCATCA AACAGCAGGG	960
AGCTAGTGGA GAGGTCTATT GTCCCAGTGG GGAAAAATGC CCTCTTGTGG GCTCCAATGT	1020
CCCCTGGGCC TTTATGCAAG GGGAAATTGC AACCATCCTT GCTGGAGATG TGAAAGTGAA	1080
AAAAGAGAGA GACTCGTGAC TTTTCCGGTT TCAGAAAAAC CCAATGATTA CCCTTAATTA	1140
AAACTGCTTG AATTGTATAT ATATCTCCAT ATATATATAT ATCCAAGACA AGGGAAATGT	1200
AGACTTCATA AACATGGCTG TATAATTTTG ATTTTTTTTG AATACATTGT GTTCTATAT	1260
TTTTTTTGAC GACAAAAGGT ATGTACTTAT AAAGACATTT TTTTCTTTTG TTAACGTTAT	1320
TAGCATATCT TTGTGCTTTA TTATCCTGGT GACAGTTACC GTTCTATGTA GGCTGTGACT	1380
TGCGCTGCTT TTTTAGAGCA CTTGGCAAAT CAGAAATGCT TCTAGCTGTA TTTGTATGCA	1440
CTTATTTTAA AAAAAAAAAA AAA	1463

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Thr Pro Thr Ser Ser Phe Val Ser Pro Pro Pro Pro Thr Ala Ser  
1 5 10 15  
Pro His Ser Asn Arg Thr Thr Pro Pro Glu Ala Ala Gln Asn Gly Gln  
20 25 30  
Ser Pro Met Ala Ala Leu Ile Leu Val Ala Asp Asn Ala Gly Gly Ser  
35 40 45  
His Ala Ser Lys Asp Ala Asn Gln Val His Ser Thr Thr Arg Arg Asn  
50 55 60  
Ser Asn Ser Pro Pro Ser Pro Ser Ser Met Asn Gln Arg Arg Leu Gly  
65 70 75 80  
Pro Arg Glu Val Gly Gly Gln Gly Ala Gly Asn Thr Gly Gly Leu Glu  
85 90 95  
Pro Val His Pro Ala Ser Leu Pro Asp Ser Ser Leu Ala Thr Ser Ala  
100 105 110  
Pro Leu Cys Cys Thr Leu Cys His Glu Arg Leu Glu Asp Thr His Phe  
115 120 125  
Val Gln Cys Pro Ser Val Pro Ser His Lys Phe Cys Phe Pro Cys Ser  
130 135 140  
Arg Gln Ser Ile Lys Gln Gln Gly Ala Ser Gly Glu Val Tyr Cys Pro  
145 150 155 160  
Ser Gly Glu Lys Cys Pro Leu Val Gly Ser Asn Val Pro Trp Ala Phe  
165 170 175  
Met Gln Gly Glu Ile Ala Thr Ile Leu Ala Gly Asp Val Lys Val Lys  
180 185 190  
Lys Glu Arg Asp Ser  
195

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2547 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CATTTTTCTG	GTCCCTCTTA	AAAGTAATCA	CTCTTAAATT	TTGTGCTTAT	TCTGTTGTTT	60
TAAAAAATAG	TTTAAACAAA	TATGTGTGTA	CTCATAAACA	TAGGTTACTT	TTGCTTCTTT	120
TTGAGATATA	TTTAAATTTT	ATTGTGGTCT	ACATATTCTT	CAGCAGTTTG	TTTTTTTACC	180
CAATATTATG	TTTCATCTGT	ATTACTGCAT	TTACTATCCC	TAGTTGATTC	ACTTCCCTGA	240
AGTACAATAT	TCAGTTGTGT	GGCTATACCA	TAATTTAGTT	ATTCATTTTG	TTGTCAGTAA	300
AATTTGGGTG	ATTATCAGAT	TTTTTTCTAG	CATGAAAAAT	GCTACTARGA	ACATTCSTGT	360
ATGTGTCTAA	TGGTATACAC	TTTCAAGTGT	TTTTTTTATAT	ATGTGAGAGT	AGATTACTTG	420
GACCTTGAAG	ATGAACATGC	TATCTTTTCC	AGATACTGCC	AATTATTTCA	GCAAGATATG	480
AGTTCCCATC	ATTTTATATT	TGTCAGCATT	TGATATTTCC	AGGCCTAGTG	ATTTCCAGTC	540
ATTTACTGGA	TATAATATGA	TTATCTCTGT	AGGGAGTTGA	TTCCATCTC	CTCAATTACT	600
AATAAAGTTA	AAAATCTTTT	CATATGTTTT	ATTGCCATTT	TTATTTCTTC	TGTAAAGTAC	660
CTACTCATGG	CTTTTTCTCA	TTTTTTGTTT	GTCATCATTG	AATTATAGGA	GTTTTGAGAG	720
AGTGAGCAAG	CTAGTCTGTG	TGTGTGTGTG	TGTGCGTGTG	TGTGTATCTC	CTTAATGTGT	780
TATATGTGAT	TGGAACCTTCT	TCTCCACCT	TGATGCTTCC	TTCTTCCCC	ACTTGTTTTA	840
GGTATCTTCT	GATGAAGTGG	AGTTATTTAT	GGTATGTTCT	CAGGAGCTAC	AATTTTAAAT	900
TTCAATATAA	TCAGTGTTTT	TAATTATCTT	ATGTTTAGCT	CTTTTGGGTC	ATGCTTAGGA	960
AATTCTTCTT	AAATTTCAAT	GATAACAGTC	TTCCATACTT	TCTTCTAAAG	TCTTATATTT	1020
TGGCCTTTCA	TATTTATTCC	TTTAATCCAM	CTGGAGTAGA	TTTTTTTTTT	CCCTCTGTAG	1080
AGTTTGGAGT	AGAGATTTTA	TTTCCTTTTT	TTTTTTTTTT	TTTTTTTCTT	TTTTTTTGAG	1140
ACAGAGTCTT	GCTCTGTCGC	CCAGGCTGGA	GTGCAGTGGC	ACTATCTCAG	CTCACTGCAA	1200
CCTCCACCTC	CTGGGTTCOA	GCGATTCTCC	TGCCTCCGCC	TCCCGAGTAG	CTGGGACTAC	1260
AGGCATGTGC	CACCACGCCC	AGCTAATTTT	TTGTATTTTT	TTTAGTAGAG	ATGGGGTTCC	1320
ACCATGTTAG	CTAGGATGAT	TTCGATTTCC	TGACCTTG TG	ATCCGCCCCG	CTCGGCCTCC	1380
CAAAATGCTG	GGATTATAGG	TGTGAGCCAC	CACGTGGCCT	CATTTCATTC	TTTCATGTGG	1440
ATAGGCAGTT	GTTCCAGAAG	TATATAGTGA	GGAGCTTCTT	CTTTCTCTAA	TGATCTGCAA	1500
TGTCACCTTC	ATCATTTATG	AAGGTTGCAC	ATATACATGG	GAATTTTTTA	GTCTGGCATT	1560
AAATGTTCTT	CAAAAGAGTT	CCTGCAAACG	TTTTTGTTTT	TATTTCTTAC	TGTTCCCTTC	1620
ACGTACTCTC	TACTGAACTA	AACTCTGTAA	TGTGTCTCGA	AACTGTCCCA	CAATTTTCCT	1680

TGTCTTAAGA GTTTAATGCT TTCATACACC TCTCACATTC AGCCTTGTGC TATTGTCTTA	1740
GGTATATTTA TTTCTCTTTT GCTCCCAATT ATGTTGTAAA CTTTTGGAAG CAGGAAGGAT	1800
ATATTGTTCA TCTTTGGTAG CATTAAACAA TGAATACAGT GTTTTTTACT TAATAGATAT	1860
TTGGTAAATC ATTGAACTAA ATTGGGGTTT GGAATTGAAG GTCTTAGAAA TTACCTGACC	1920
ACTCCCATTA TATTTGCCCA TCCATGATCA CTGAGATTTA TAGAGATTAG ATGCAATGCC	1980
CAGTTTCACA TATGTTTTTG CATCACTGTC TCTTTTTTTC TTGAGCTTAT TCCAGAGTGT	2040
CTTTTAATAT CCATTCCATG ATCAAATGGC TGAACTATTA AAATGCTGTC CAGAAGTGTA	2100
AAGCAATATG AAGATGCTAG AAAAGTTGAA GAGACACATA TATGGTAGGT CCAAGACCAT	2160
TACACTTACT GAGTCCATTA CTAAAAATGA TGTTCACCTA ACATCAAAAC ACTCAGGATT	2220
ACCCAAGCAC AATATACTGA TTTGCACCTC TGCCTTTGTT CATGCCCTT GTTCAGGAGA	2280
ACTGCTTTCA TGTGCTACTG TCCATAGATC TTCTCTATCC TTACAGATTA ATTTCTTCCT	2340
TTTGAATGCT ATGTTTCCAT ACTTTGACAT TCCTTCTGCA CCATTCAGAC CATATTTTAG	2400
TTCTTTTTTA TGGTATCTCT CACTTTTGAT TGTCACCCCT TAAGTCAAAG ACAATTTTTT	2460
CATCTGTGTC TTCTCAACAC CCAGCACAGG GCTATGTTTG GTAAAAATTA GGTATCCAAG	2520
ATGTACTAAA TGAAAAAAAA AAAAAAA	2547

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met	Phe	Phe	Lys	Arg	Val	Pro	Ala	Asn	Val	Phe	Val	Phe	Ile	Ser	Tyr
1				5					10					15	
Cys	Ser	Leu	His	Val	Leu	Ser	Thr	Glu	Leu	Asn	Ser	Val	Met	Cys	Leu
			20					25					30		
Glu	Thr	Val	Pro	Gln	Phe	Ser	Leu	Ser							
		35					40								

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2245 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GCTCAACGGC CTCTTCTGGT TGCTGTCTTC CTCGTCCCTC CGGCCCTTCT TCCTACTCAG	60
CGTCTCACTT TTGGCCTATT TTCTGCTGGA TCTCTGGCAG CCTCGCTTTC TCCCTGACGT	120
TTCAGCATCA TCCCCAGAGG AGCCCACTC TGACAGTGAG GGTGCGGGGT CAGGCGCCCG	180
GCCGCACCTG CTGAGTGTGC CCGAGTTGTG CAGATACCTG GCTGAGAGCT GGCTCACCTT	240
CCAGATTCAC CTGCAGGAGC TGCTGCAGTA CAAGAGGCAG AATCCAGCTC AGTTCTGCGT	300
TCGARTCTGC TCTGGCTGTG CTGTGTTGGC TGTGTTGGGA CACTATGTTT CAGGGATTAT	360
GATTTCTAC ATTGTCTTGT TGAGTATCCT GCTGTGGCCC CTGGTGGTTT ATCATGARCT	420
GATCCAGAGG ATGTWCACTC GCCTGGAGCC CCTGCTCATG CAGCTGGACT ACAGCATGAA	480
GGCAGAAKCC AATGCCCTGC ATCACAAACA CGACAAGAGG AAGCGTCAGG GGAAGAATGC	540
ACCCCCAGGA GGTGATGAGC CACTGGCAGA GACAGAGAGT GAAAGCGAGG CAGAGCTGGC	600
TGGCTTCTCC CCAGTGGTGG ATGTGAAGAA AACAGCATTG GCCTTGGCCA TTACAGACTC	660
AGAGCTGTCA GATGAGGAGG CTTCTATCTT GGAGAGTGGT GGCTTCTCCG TATCCCGGGC	720
CACAACTCCG CAGCTGACTG ATGTCTCCGA GGATTTGGAC CAGCAGAGCC TGCCAAGTGA	780
ACCAGAGGAG ACCCTAAGCC GGGACCTAGG GGAGGGAGAG GAGGGAGAGC TGGCCCCCTCC	840
CGAAGACCTA CTAGGCCGTC CTCAAGCTCT GTCAAGGCAA GCCCTGGACT TGGAGGAAGA	900
GGAAGAGGAT GTGGCAGCTA AGGAAACCTT GTTGC GGCTC TCATCCCCC TCCACTTTGT	960
GAACACGCAC TTCAATGGGG CAGGGTCCCC CCCAGATGGA GTGAAATGCT CCCCTGGAGG	1020
ACCAGTGGAG AACTGAGCC CCGAGACAGT GAGTGGTGGC CTCACTGCTC TGCCCGGCAC	1080
CCTGTCACTT CCACTTTGCC TTGTTGGAAG TGACCCAGCC CCCTCCCCTT CCATTCTCCC	1140
ACCTGTTCCC CAGGACTCAC CCCAGCCCCT GCCTGCCCCCT GAGGAAGAAG AGGCACTCAC	1200
CACTGAGGAC TTTGAGTTGC TGGATCAGGG GGAGCTGGAG CAGCTGAATG CAGAGCTGGG	1260
CTTGAGCCA GAGACACCGC CAAAACCCCC TGATGCTCCA CCCCTGGGGC CCGACATCCA	1320
TTCTCTGGTA CAGTCAGACC AAGAAGCTCA GGCCGTGGCA GAGCCATGAG CCAGCCGTTG	1380

AGGAAGGAGC	TGCAGGCACA	GTAGGGCTTC	CTGGCTAGGA	GTGTTGCTGT	TTCTCCTTT	1440
GCCTACCACT	CTGGGGTGGG	GCAGTGTGTG	GGGAAGCTGG	CTGTCGGATG	GTAGCTATTC	1500
CACCYTCTGC	CTGCCTGCCT	GCCTGCTGTC	CTGGGCATGG	TGCAGTACCT	GTGCCTAGGA	1560
TTGGTTTTAA	ATTTGTAAAT	AATTTTCCAT	TTGGGTTAGT	GGATGTGAAC	AGGGCTAGGG	1620
AAGTCCTTCC	CACAGCCTGC	GCTTGCCTCC	CTGCCTCATC	TCTATTCTCA	TTCCACTATG	1680
CCCAAGCCC	TGGTGGTCTG	GCCCTTTCTT	TTTCCTCCTA	TCCTCAGGGA	CCTGTGCTGC	1740
TCTGCCCTCA	TGTCCCACTT	GGTTGTTTAG	TTGAGGCACT	TTATAATTTT	TCTCTTGTCT	1800
TGTGTTCCCT	TCTGCTTTAT	TTCCCTGCTG	TGTCCTGTCC	TTAGCAGCTC	AACCCCATCC	1860
TTTGCCAGCT	CCTCCTATCC	CGTGGGCACT	GGCCAAGCTT	TAGGGAGGCT	CCTGGTCTGG	1920
GAAGTAAAGA	GTAAACCTGG	GGCAGTGGGT	CAGGCCAGTA	GTTACACTCT	TAGGTCACTG	1980
TAGTCTGTGT	AACCTTCACT	GCATCCTTGC	CCCATTCAAG	CCGGCCTTTC	ATGATGCAGG	2040
AGAGCAGGGA	TCCCGCAGTA	CATGGCGCCA	GCACTGGAGT	TGGTGAGCAT	GTGCTCTYTY	2100
TTGAGATTAG	GAGCTTCCTT	ACTGCTCCTC	TGGGTGATCC	AAGTGTAGTG	GGACCCCTTA	2160
CTAGGGTCAG	GAAGTGGACA	CTAACATCTG	TGCAGGTGTT	GACTTGAAAA	ATAAAGTGTT	2220
GATTGGCTAG	AAAAAAAAAA	AAAAA				2245

(2) INFORMATION FOR SEO ID NO:17:

(ii) MOLECULE TYPE: protein

Met Ile Ser Tyr Ile Val Leu Leu Ser Ile Leu Leu Trp Pro Leu Val  
1 5 10 15

Ala Gly Phe Ser Pro Val Val Asp Val Lys Lys Thr Ala Leu Ala Leu  
 85 90 95  
 Ala Ile Thr Asp Ser Glu Leu Ser Asp Glu Glu Ala Ser Ile Leu Glu  
 100 105 110  
 Ser Gly Gly Phe Ser Val Ser Arg Ala Thr Thr Pro Gln Leu Thr Asp  
 115 120 125  
 Val Ser Glu Asp Leu Asp Gln Gln Ser Leu Pro Ser Glu Pro Glu Glu  
 130 135 140  
 Thr Leu Ser Arg Asp Leu Gly Glu Gly Glu Glu Gly Glu Leu Ala Pro  
 145 150 155 160  
 Pro Glu Asp Leu Leu Gly Arg Pro Gln Ala Leu Ser Arg Gln Ala Leu  
 165 170 175  
 Asp Leu Glu Glu Glu Glu Glu Asp Val Ala Ala Lys Glu Thr Leu Leu  
 180 185 190  
 Arg Leu Ser Ser Pro Leu His Phe Val Asn Thr His Phe Asn Gly Ala  
 195 200 205  
 Gly Ser Pro Pro Asp Gly Val Lys Cys Ser Pro Gly Gly Pro Val Glu  
 210 215 220  
 Thr Leu Ser Pro Glu Thr Val Ser Gly Gly Leu Thr Ala Leu Pro Gly  
 225 230 235 240  
 Thr Leu Ser Pro Pro Leu Cys Leu Val Gly Ser Asp Pro Ala Pro Ser  
 245 250 255  
 Pro Ser Ile Leu Pro Pro Val Pro Gln Asp Ser Pro Gln Pro Leu Pro  
 260 265 270  
 Ala Pro Glu Glu Glu Glu Ala Leu Thr Thr Glu Asp Phe Glu Leu Leu  
 275 280 285  
 Asp Gln Gly Glu Leu Glu Gln Leu Asn Ala Glu Leu Gly Leu Glu Pro  
 290 295 300  
 Glu Thr Pro Pro Lys Pro Pro Asp Ala Pro Pro Leu Gly Pro Asp Ile  
 305 310 315 320  
 His Ser Leu Val Gln Ser Asp Gln Glu Ala Gln Ala Val Ala Glu Pro  
 325 330 335

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1406 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double



(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CTTGTGGGAA GAGCTGAAGC AGGCGCTCTT GGCTCGGCGC GGCCCGCTGC AATCCGTGGA	60
GGAACGCGCC GCCGAGCCAC CATCATGCCT GGGCACTTAC AGGAAGGCTT CGGCTGCGTG	120
GTCACCAACC GATTGACCA GTTATTGAC GACGAATCGG ACCCCTTCGA GGTGCTGAAG	180
GCAGCAGAGA ACAAGAAAAA AGAAGCCGGC GGGGGCGGCG TTGGGGGCCC TGGGGCCAAG	240
AGCGCAGCTC AGGCCGCGGC CCAGACCAAC TCCAACGCGG CAGGCAAACA GCTGCGCAAG	300
GAGTCCCAGA AAGACCGCAA GAACCCGCTG CCCCCAGCG TTGGCGTGGT TGACAAGAAA	360
GAGGAGACGC AGCCGCCCCG GCGCTTAAG AAAGAAGGAA TAAGACGAGT TGGGAAGAAGA	420
CCTGATCAAC AACTTCAGGG TGAAGGGAAA ATAATTGATA GAAGACCAGA AAGGCGACCA	480
CCTCGTGAAC GAAGATTGTA AAAGCCACTT GAAGAAAAGG GTGAAGGAGG CGAATTTTCA	540
GTTGATAGAC CGATTATTGA CCGACCTATT CGAGGTCGTG GTGGTCTTGG AAGAGGTCGA	600
GGGGGCCGTG GACGTGGAAT GGGCCGAGGA GATGGATTG ATTCTCGTGG CAAACGTGAA	660
TTTGATAGGC ATAGTGGAAG TGATAGATCT TCTTTTTCAC ATTACAGTGG CCTGAAGCAC	720
GAGGACAAAC GTGGAGGTAG CGGATCTCAC AACTGGGGAA CTGTCAAAGA CGAATTAACT	780
GACTTGATC AATCAAATGT GACTGAGGAA ACACCTGAAG GTGAAGAACA TCATCCAGTG	840
GCAGACACTG AAAATAAGGA GAATGAAGTT GAAGAGGTAA AAGAGGAGGG TCCAAAAGAG	900
ATGACTTTGG ATGAGTGGA GGCTATTCAA AATAAGGACC GGGCAAAGT AGAATTTAAT	960
ATCCGAAAAC CAAATGAAGG TGCTGATGGG CAGTGAAGA AGGGATTTGT TCTTCATAAA	1020
TCAAAGAGTG AAGAGGCTCA TGCTGAAGAT TCGGTTATGG ACCATCATTT CCGGAAGCCA	1080
GCAAATGATA TAACGTTTCA GCTGGAGATC AATTTTGGAG ACCTTGCCG CCCAGGACGT	1140
GGCGGCAGGG GAGGACGAGG TGGACGTGGG CGTGGTGGGC GCCCAAACCG TGGCAGCAGG	1200
ACCGACAAGT CAAGTGCTTT TGCTCCTGAT GTGGATGACC CAGAGGCATT CCCAGTTTTG	1260
GCTTAAMTGG ATGCCATAAG ACAACCCTGG TTCCTTTGTG AACCCTTTTG TTCAAAGCTT	1320
TTGCATGCTT AAGGATTCCA AACGACTAAG AAATTAAAAA AAAAAAAAAA AAAAAAAAAA	1380
AAAAAAAAA AAAAAAAAAA AAAAAA	1406

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met	Pro	Gly	His	Leu	Gln	Glu	Gly	Phe	Gly	Cys	Val	Val	Thr	Asn	Arg	
1				5					10					15		
Phe	Asp	Gln	Leu	Phe	Asp	Asp	Glu	Ser	Asp	Pro	Phe	Glu	Val	Leu	Lys	
			20					25					30			
Ala	Ala	Glu	Asn	Lys	Lys	Lys	Glu	Ala	Gly	Gly	Gly	Gly	Val	Gly	Gly	
			35				40						45			
Pro	Gly	Ala	Lys	Ser	Ala	Ala	Gln	Ala	Ala	Ala	Gln	Thr	Asn	Ser	Asn	
	50					55					60					
Ala	Ala	Gly	Lys	Gln	Leu	Arg	Lys	Glu	Ser	Gln	Lys	Asp	Arg	Lys	Asn	
65					70					75					80	
Pro	Leu	Pro	Pro	Ser	Val	Gly	Val	Val	Asp	Lys	Lys	Glu	Glu	Thr	Gln	
				85					90					95		
Pro	Pro	Val	Ala	Leu	Lys	Lys	Glu	Gly	Ile	Arg	Arg	Val	Gly	Arg	Arg	
			100					105					110			
Pro	Asp	Gln	Gln	Leu	Gln	Gly	Glu	Gly	Lys	Ile	Ile	Asp	Arg	Arg	Pro	
		115					120					125				
Glu	Arg	Arg	Pro	Pro	Arg	Glu	Arg	Arg	Phe	Glu	Lys	Pro	Leu	Glu	Glu	
	130					135					140					
Lys	Gly	Glu	Gly	Gly	Glu	Phe	Ser	Val	Asp	Arg	Pro	Ile	Ile	Asp	Arg	
145					150					155					160	
Pro	Ile	Arg	Gly	Arg	Gly	Gly	Leu	Gly	Arg	Gly	Arg	Gly	Gly	Arg	Gly	
				165					170					175		
Arg	Gly	Met	Gly	Arg	Gly	Asp	Gly	Phe	Asp	Ser	Arg	Gly	Lys	Arg	Glu	
			180					185					190			
Phe	Asp	Arg	His	Ser	Gly	Ser	Asp	Arg	Ser	Ser	Phe	Ser	His	Tyr	Ser	
		195					200					205				
Gly	Leu	Lys	His	Glu	Asp	Lys	Arg	Gly	Gly	Ser	Gly	Ser	His	Asn	Trp	
	210					215					220					
Gly	Thr	Val	Lys	Asp	Glu	Leu	Thr	Asp	Leu	Asp	Gln	Ser	Asn	Val	Thr	
225					230					235					240	

Glu Glu Thr Pro Glu Gly Glu Glu His His Pro Val Ala Asp Thr Glu  
 245 250 255  
 Asn Lys Glu Asn Glu Val Glu Glu Val Lys Glu Glu Gly Pro Lys Glu  
 260 265 270  
 Met Thr Leu Asp Glu Trp Lys Ala Ile Gln Asn Lys Asp Arg Ala Lys  
 275 280 285  
 Val Glu Phe Asn Ile Arg Lys Pro Asn Glu Gly Ala Asp Gly Gln Trp  
 290 295 300  
 Lys Lys Gly Phe Val Leu His Lys Ser Lys Ser Glu Glu Ala His Ala  
 305 310 315 320  
 Glu Asp Ser Val Met Asp His His Phe Arg Lys Pro Ala Asn Asp Ile  
 325 330 335  
 Thr Phe Gln Leu Glu Ile Asn Phe Gly Asp Leu Gly Arg Pro Gly Arg  
 340 345 350  
 Gly Gly Arg Gly Gly Arg Gly Gly Arg Gly Arg Gly Gly Arg Pro Asn  
 355 360 365  
 Arg Gly Ser Arg Thr Asp Lys Ser Ser Ala Phe Ala Pro Asp Val Asp  
 370 375 380  
 Asp Pro Glu Ala Phe Pro Val Leu Ala  
 385 390

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4237 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GCGGACGCGG CCAGTCAGGT GTCCTGGGC TCCGGTCTCA CCATCCTGTC CCAGCCGCTC 60  
 ATGTACGTGA AAGTGCTCAT CCAGGTGGGA TATGAGCCTC TTCCTCCAAC AATAGGACGA 120  
 AATATTTTGG GCGGCAAGT GTGTCAGCTT CCTGGTCTCT TTAGTTATGC TCAGCACATT 180  
 GCCAGTATCG ATGGGAGGCG CGGGTTGTTC ACAGGCTTAA CTCCAAGACT GTGTTCGGGA 240  
 GTCCTTGGA CTGTGGTCCA TGGTAAAGTT TTACAGCATT ACCAGGAGAG TGACAAGGGT 300  
 GAGGAGTTAG GAMCTGAAAA TGTACARAAA GAAGTCTCAT CTTCTTTGA MCACGTTATC 360

AAGGAGACAA CTCGAGAGAT GATCGCTCGT TCTGCTGCTA CCCTCATCAC ACATCCCTTC	420
CATGTTGATC ACTCTGAGAT CTATGGTACA RTTCATTGGC AGAGAATCCA AGTACTGTGG	480
ACTTTGTGAT TCCATAATAA CCATCTATCG GGAAGAGGGC ATTCTAGGAT TTTTCGCGGG	540
TCTTGTTCTT CGCCTTCTAG GTGACATCCT TTCTTTGTGG CTGTGTAAC TACTGGCCTA	600
CCTCGTCAAT ACCTATGCAC TGGACAGTGG GGTTCCTACC ATGAATGAAA TGAAGAGTTA	660
TTCTCAAGCT GTCACAGGAT TTTTTCGAG TATGTTGACC TATCCCTTTG TGCTTGTCTC	720
CAATCTTATG GCTGTCAACA ACTGTGGTCT TGCTGGTGGA TGCCCTCCTT ACTCCCCAAT	780
ATATACGTCT TGGATAGACT GTTGGTGCAT GCTACAAAAA GAGGGGAATA TGAGCCGAGG	840
AAATAGCTTA TTTTTCGGA AGGTCCCCTT TGGGAAGACT TATTGTTGTG ACCTGAAAAAT	900
GTTAATTTGA AGATGTGGGG CAGGGACAGT GACATTTCTG TAGTCCCAGA TGCACAGAAT	960
TATGGGAGAG AATGTTGATT TCTATACAGT GTGGCGCGCT TTTTAAATAA TCATTTAATC	1020
TTGGGAAAAAT TCAGGTGTTT GGTGTCTGCC TTTTGTTC TTTTTCAG CACAACATAA	1080
CTTACCACTG AACTCCCCC TTTAGTTATT CTGAATTAGG ATATTTTTCG TCCAAATTCT	1140
TATTTTACTT AACCAGAAGG GAAAAAAGT TGTATTTTCC TGAAGCTACA GGCACTTTGT	1200
CATGTGATTT TTGAGTCTCA ATTTAAGGCT TTGTAAAATG AAGAGTAGAA TTCCAAGAAA	1260
AATGAGAAAT AATTTTGTAA AACTTAACAA AATCACTAAA TTAACTATA TGGGAGGTTA	1320
TGAATTACTT TTTCTTGGGT AGACCCTAAA ATGTCAGTAG CATGCACCAG AATCTGACTC	1380
CCATTATGCT TCTAAGCACA TTTCAATTGAC CTTGTCTCTC AACTTCAAG AAAAGGACAG	1440
TACATTGCTA CATTACCCTA GAAAGTCTGT GTGAGGATCT GCCCCTTCAG TCTGTTATTG	1500
CAAAGTAATA AAATGTCACC TACAGGGAGC CTCTGAGCCT ACTCTAGTTC AAGAGGCTAC	1560
CTGAAAAAAA ATAAATAAGA TAAAGGGTCA GCAACAACAA AGAAAAAGAC AATTACAGAA	1620
AATAAGCAAG ATTTGGAAAG GAAGTATAAT GGCACTTTTT TCCTCAAAGG AAGTTCTTGT	1680
TTTCACATAA AATATGAAAA GCAGATCCTG CAGGAGTAAC CCCCTTCTTT AAGAGCCAAG	1740
TATTTGCCAG TGCTTAAATT ACACCATACC GTTCTAATTA TATATAATCT TTTGTTCTTC	1800
AGTTTTTTGT TTTGTTTCCT TTTTGTATT GTTGCCGAAG GTGAGTAGTT TTGCATTTCT	1860
GATGACAGCC TTGGAAAGTA TATTTGTAAC TCCATGTCTG GTAATGCCAA CCCAAGTCGA	1920
CATGGGTCTT AGGACACTGA CCACCTCACA TGCCATACCC TCAGTTAAGC ATGTTAACAT	1980
TTATAGGAGG AAAAAAATCA CTTTGGGAGA AAATAAAATT CAACTCAAGC ATAAAGCTTC	2040
TGTTTACTCA GGCCTTCTAA AAAGCAGGTT AAAATGCTCT AAAATGAGAA AGCCTGTGGT	2100

TTCAC TTATT TATATAACTC ACTGGGACAT TGCCAAATGA GTAAGCACTT AATTCGCTGC 2160  
TTCTGAGACT TCTCTGTCAA AACAGCCCCA CTGATAATAT TAGACAGAAC GAGAATGCAG 2220  
GGGTCTCTTC CCTCCCCTGG GGTTTAGGAA GCTCATGAGG AGCTCGGCTT AAAATGTCTT 2280  
TGATGTCTCT TCCTTTGTCT CAAAAAGTAA TGTCAATTTT ATATACTATT TCAATATTAC 2340  
TATCTGCATT TGTTTTAATA TAAAAATGTT TGCTGCCTAC CTTTTTCTCC CAAAAATCT 2400  
TTAAGTAAAG ATGATCTGGG AAAATGAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 2460  
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 2520  
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 2580  
AAAAAAAAAA AAAAAAAGC GGCCGCAGGT CTAGAATTCA ATCGGAAGGT ATATAGCTTA 2640  
TTTGTGTGCTT TTCATTGTAA TTTAACATGG TTAATGGTTA ATTACTATTT AACACACATT 2700  
TCAAATGAAT ATTATTTGGG GGATTAGATT GAGTGAAATT AACCTGCTAT TAAATAGTAA 2760  
ACTTTTCCTC TGGAGTCACT TTTTCCCCC TTCAAAGTAT GTTACTGAGG AAGTAACTT 2820  
TTTTTTTTTT TTTTGGTTTT TGTTTTTTGA GACACAGTCT CGCTCTGTTG CCCAGGCTGC 2880  
TGGAGTGCCG TGGCGCAATC TCGGCTCACT GCAACCTCCG CCTCCTGGAT TCAAACAATT 2940  
CTCCTGCTTC AGCCTCCTGA GTAGCTGGGA TTACAGGCAC ATGCCACCAC GCCCGGCTAA 3000  
TTTTTGATTT TTTAGTAGAG ACTGGGTTTC ACCATGTTGG TCAGGCTGGT CTCAAACCTC 3060  
TGACCTCGTG ATCCACCCGC CTCGGCCTCC CAAAATCCTG GGATTACAGG CGCGAGCCAC 3120  
CACACCCGGC TGGAAGTAAA CATTTTTTAAA GCTACTTTTA CTCATTCTAG CTTGTAGAA 3180  
TGACCATTGC AGCTTGAGGG ACCTAGTTCT TACCTTTTCT TGCAACCAAC AACTTGCAA 3240  
TTGTGTCTGG TATGCTTGTT CCTGCTGCTA ATAAAGTAAG GCCCATTACT GTATCGGGAA 3300  
TTTCTAGTGT TTCCCCTGTA ATAAACAGAT ATTTCAAGTT ACAAATCTTA AAGATTCACT 3360  
AACCATCCTT TGCAGTTATT TTGGATATTT CCTTCGTGAA CAAAAATAAA ATAGGCACAT 3420  
TTAGAATTCA GAGCCAATAT GTGCTTGCTT ATTAGTTTTT TAGCTAGCAA CATATTTGAA 3480  
TCAGGCTGGT AATTCGGGTA ACCCAGGTAG CACAGATTTT TAATGACATA TYTAAAGATA 3540  
CGTAACAGCT AAAATTTCTG CCAGTGAGAA ATTTTCCTGT TTGATATTTT TTACAAAAGA 3600  
TGTTTATGTC CACCATTATY TTCATTCAGG GGCTGTGCTG AATATTTGAT AATGAGACTG 3660  
ATCATTCGCG TTTTCTTTT TTAATAATAT TAGGCAGAGT TAAGCAAATT AATTATAGCT 3720  
ATCTTTAAGC TATAAATGTG TTAACATGTA TATATACCAT TTATTATGTT CTACTTTAGT 3780

GATATACCTT AATTAGTGG GCTTTGGCAG GCGGGGGGAG GGGGAACGTT CATTAATCTC	3840
TGAGGAAAAAC AAAACCTGTT TTCTACTTGA GTCTAACATA TGGTCCCAAT TTATTAATAC	3900
TTCTGTAAAA TTTGATGTCA GGTCAACATT TTTCAGAAAT GTATTTATTC TCAGAAACAG	3960
AACCAGAGAG AAGTTAAACA AAAGGTTATG TAACTGTTCC TTTAATGTTG TAATTGAAAA	4020
CTTGGTTTAG CGTCTTTTTT TTCTTTCTCT TTTTTTTTCT TAAAATGCCA ACTAAAATAA	4080
TTAGAAAAGTA GCTTATTTAT TGCATGCTTA TACATTGATA TTGGAATTGG AATTGGTTGT	4140
TAATTTCTGT TACTGGCTTT GCTAGAATTC ATATGTGCAT AAATAACACT AATATTTATC	4200
ATCTTGAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAA	4237

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met	Tyr	Ile	Tyr	His	Leu	Leu	Cys	Ser	Thr	Leu	Val	Ile	Tyr	Leu	Asn
1				5				10					15		
Leu	Val	Gly	Phe	Gly	Arg	Ala	Gly	Glu	Gly	Glu	Arg	Ser	Leu	Ile	Ser
		20					25						30		
Glu	Glu	Asn	Lys	Thr	Cys	Phe	Leu	Leu	Glu	Ser	Asn	Ile	Trp	Ser	Gln
		35					40					45			
Phe	Ile	Asn	Thr	Ser	Val	Lys	Phe	Asp	Val	Arg	Ser	Thr	Phe	Phe	Arg
	50					55				60					
Asn	Val	Phe	Ile	Leu	Arg	Asn	Arg	Thr	Arg	Glu	Lys	Leu	Asn	Lys	Arg
65				70					75					80	
Leu	Cys	Asn	Cys	Ser	Phe	Asn	Val	Val	Ile	Glu	Asn	Leu	Val		
			85						90						

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TNTTGAAGACT GTTGCTTGTT TGGAATGT

29

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CNCCATCTAAT GGGATGATGG GTTCTTGA

29

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ANTTTCCGTCA CCTCGTTCGC CTGCTGCT

29

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GNATACGAGGG GTTCCCATGG CTTCTTCT

29

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TNTACGACGAC ATCCAACAAT CACACTGG

29

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TNGTCCGGTTG GAATGAGGTG AGGCAGTG

29

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GNTCCTCACTA TATACTTCTG GAACAACT

29

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single



(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GNCCTAAGAGT GTAACTACTG GCCTGACC

29

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TNTCCTCGTGC TTCAGGCCAC TGTAATGT

29

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ANGCCCACTAA ATTAAGGTAT ATCACTAA

29

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met Trp Gly Leu Gly Thr Thr Ser Ser Phe Arg Trp Tyr Ser Ser Asp

1	5	10	15
Tyr Arg Arg Ser Phe Gln Leu Asn Ser Pro Val Asp Lys Met Arg Lys			
20	25	30	
Thr Gly Glu Gln Ala Phe Ser Val Phe Thr Tyr Lys Val Arg Ser Val			
35	40	45	
Met Gly Gln			
50			

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2199 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO33:

AGTTGGCAGG TGGAGAGGCA GGTGTTGGGAGG GAAAGTCGGG GGAGGACGCG GAAGAGGAGC	60
TGTGGGAAGG GGGAGGAGGG AGGGAGGAAA AGAGGAGGAG GCGGAGGAGA ACTGAGCAGA	120
GCAGAGCATC GAGCCAAAGG GGAGATGAGT TTGTCTGTCC TCTGCTGAGG CTACGGCCGG	180
GCCTAGGGAA CTGGGAGCTT GGGTGGGAAGC GACACCCGTG GAAGTGGGAG GAGGTGGCGC	240
CGGGACTTTA ACCCCTTGTG GGCTCTGCGG CAGGGGATTT AACCCTTTGT GGATCTGGCC	300
CCTCGGAGGC AGCGTCATCG GTAGTTTTAA CCCCTTCGGG GCTGGGTTC ACGCACTGGA	360
CTTACCCTCA TCACCTTGCT CACCAACTCC TTTATTGGGG TGCTCCGCTT GGAGGTTTGA	420
GGCCACCTC CGCCATTAC GTACTGTTCC TGCCGCTGCA CCCCCTTGGA CCCGCTAGCT	480
GGCCGCACTG TGGGCGCTTA ACCCTTTACT GACTTGAGCT CCCAGATTG CAGTTGGAGT	540
TTGCTGATAG AAGGACTAGC TAAAGGCGTC ACTGCAGGAA TTACAACTG AAGAGGACTC	600
TGTTGGACTG TTTTTTTTTT CTTTTTCTTT TTTTAAAGAA AAACCCATTT TTTTCCTTAA	660
GGACTTACTA GCCAAAATTT CTAAACTTC GAGGACTCTA CTAGCCATGG CCGAGCCATT	720
CTTGTCAGAA TATCAACACC AGCCTCAAAC TAGCAACTGT ACAGGTGCTG CTGCTGTCCA	780
GGAAGAGCTG AACCTGAGC GCCCCCAGG CGCGGAGGAG CGGGTGCCCG AGGAGGACAG	840
TAGGTGGCAA TCGAGAGCGT TCCCCAGTT GGGTGGCCGT CCGGGGCCGG AGGGGGAAGG	900
GAGCCTGGAA TCCCAACCAC CTCCCTTGCA GACCCAGGCC TGTCCAGAAT CTAGCTGCCT	960

GAGAGAGGGC GAGAAGGGCC AGAATGGGGA CGACTCGTCC GCTGGCGGCG ACTTCCCGCC	1020
GCCGGCAGAA GTGGAACCGA CGCCCGAGGC CGAGCTGCTC GCCCAGCCTT GTCATGACTC	1080
CGAGGCCAGT AAGTTGGGGG CTCCTGCCGC AGGGGGCGAA GAGGAGTGGG GACAGCAGCA	1140
GAGACAGCTG GGGAAGAAAA AACATAGGAG ACGCCCGTCC AAGAAGAAGC GGCATTGGAA	1200
ACCGTACTAC AAGCTGACCT GGGAAAGAGAA GAAAAAGTTC GACGAGAAAC AGAGCCTTCG	1260
AGCTTCAAGG ATCCGAGCCG AGATGTTCGC CAAGGGCCAG CCGGTCGCGC CCTATAACAC	1320
CACGCAGTTC CTCATGGATG ATCACGACCA GGAGGAGCCG GATCTCAAAA CCGGCCTGTA	1380
CTCCAAGCGG GCCGCCGCCA AATCCGACGA CACCAGCGAT GACGACTTCA TGGAAGAAGG	1440
GGGTGAGGAG GATGGGGGCA GCGATGGGAT GGGAGGGGAC GGCAGCGAGT TTCTGCAGCG	1500
GGACTTCTCG GAGACGTACG AGCGGTACCA CACGGAGAGC CTGCAGAACA TGAGCAAGCA	1560
GGAGCTCATC AAGGAGTACC TGGAACTGGA GAAGTGCTTC TCGCGCATGG AGGACGAGAA	1620
CAACCGGCTG CGGCTGGAGA GCAAGCGGCT GGGTGGCGAC GACGCGCGTG TCGGGGAGCT	1680
GGAGCTGGAG CTGGACCGGC TGC GCGCCGA GAACCTCCAG CTGCTGACCG AGAACGAACT	1740
GCACCGGCAG CAGGAGCGAG CGCCGCTTTC CAAGTTTGGA GACTAGACTG AAACCTTTTTT	1800
GGGGGAGGGG GCAAAGGGGA CTTTTTACAG TGATGGAATG TAACATTATA TACATGTGTA	1860
TATAAGACAG TGGACCTTTT TATGACACAT AATCAGAAGA GAAATCCCCC TGGCTTTGGT	1920
TGGTTTCGTA AATTTAGCTA TATGTAGCTT GCGTGCTTTC TCCTGTTCTT TTAATTATGT	1980
GAAACTGAAG AGTTGCTTTT CTTGTTTTC TTTT TAGAAG TTTTTTTCCT TAATGTGAAA	2040
GTAATTTGAC CAAGTTATAA TGCATTTTTG TTTT TAACAA ATCCCCTCCT TAAACGGAGC	2100
TATAAGGTGG CCAAATCTGA GAACAATTAA ATTCATTTTA GTTATAATAA ATTTAATATT	2160
TGTAAATGTA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	2199

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met Ala Glu Pro Phe Leu Ser Glu Tyr Gln His Gln Pro Gln Thr Ser

1		5		10		15											
Asn	Cys	Thr	Gly	Ala	Ala	Ala	Val	Gln	Glu	Glu	Leu	Asn	Pro	Glu	Arg		
			20					25					30				
Pro	Pro	Gly	Ala	Glu	Glu	Arg	Val	Pro	Glu	Glu	Asp	Ser	Arg	Trp	Gln		
		35					40					45					
Ser	Arg	Ala	Phe	Pro	Gln	Leu	Gly	Gly	Arg	Pro	Gly	Pro	Glu	Gly	Glu		
	50					55					60						
Gly	Ser	Leu	Glu	Ser	Gln	Pro	Pro	Pro	Leu	Gln	Thr	Gln	Ala	Cys	Pro		
65					70					75					80		
Glu	Ser	Ser	Cys	Leu	Arg	Glu	Gly	Glu	Lys	Gly	Gln	Asn	Gly	Asp	Asp		
				85					90					95			
Ser	Ser	Ala	Gly	Gly	Asp	Phe	Pro	Pro	Pro	Ala	Glu	Val	Glu	Pro	Thr		
			100					105					110				
Pro	Glu	Ala	Glu	Leu	Leu	Ala	Gln	Pro	Cys	His	Asp	Ser	Glu	Ala	Ser		
		115					120					125					
Lys	Leu	Gly	Ala	Pro	Ala	Ala	Gly	Gly	Glu	Glu	Glu	Trp	Gly	Gln	Gln		
	130					135					140						
Gln	Arg	Gln	Leu	Gly	Lys	Lys	Lys	His	Arg	Arg	Arg	Pro	Ser	Lys	Lys		
145					150					155					160		
Lys	Arg	His	Trp	Lys	Pro	Tyr	Tyr	Lys	Leu	Thr	Trp	Glu	Glu	Lys	Lys		
				165					170					175			
Lys	Phe	Asp	Glu	Lys	Gln	Ser	Leu	Arg	Ala	Ser	Arg	Ile	Arg	Ala	Glu		
			180					185					190				
Met	Phe	Ala	Lys	Gly	Gln	Pro	Val	Ala	Pro	Tyr	Asn	Thr	Thr	Gln	Phe		
		195					200					205					
Leu	Met	Asp	Asp	His	Asp	Gln	Glu	Glu	Pro	Asp	Leu	Lys	Thr	Gly	Leu		
	210					215					220						
Tyr	Ser	Lys	Arg	Ala	Ala	Ala	Lys	Ser	Asp	Asp	Thr	Ser	Asp	Asp	Asp		
225					230					235					240		
Phe	Met	Glu	Glu	Gly	Gly	Glu	Glu	Asp	Gly	Gly	Ser	Asp	Gly	Met	Gly		
				245					250					255			
Gly	Asp	Gly	Ser	Glu	Phe	Leu	Gln	Arg	Asp	Phe	Ser	Glu	Thr	Tyr	Glu		
			260					265					270				
Arg	Tyr	His	Thr	Glu	Ser	Leu	Gln	Asn	Met	Ser	Lys	Gln	Glu	Leu	Ile		
		275					280					285					
Lys	Glu	Tyr	Leu	Glu	Leu	Glu	Lys	Cys	Leu	Ser	Arg	Met	Glu	Asp	Glu		
	290					295					300						
Asn	Asn	Arg	Leu	Arg	Leu	Glu	Ser	Lys	Arg	Leu	Gly	Gly	Asp	Asp	Ala		
305					310					315					320		

Arg Val Arg Glu Leu Glu Leu Glu Leu Asp Arg Leu Arg Ala Glu Asn  
325 330 335

Leu Gln Leu Leu Thr Glu Asn Glu Leu His Arg Gln Gln Glu Arg Ala  
340 345 350

Pro Leu Ser Lys Phe Gly Asp  
355

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1851 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GGCTAGGCCG CGAGCTTAGT CCTGGGAGCC GCCTCCGTCG CCGCCGTCAG AGCCGCCCTA	60
TCAGATTATC TTAACAAGAA AACCAACTGG AAAAAAAAAAT GAAATTCCTT ATCTTCGCAT	120
TTTTCGGTGG TGTTACCTT TTATCCCTGT GCTCTGGGAA AGCTATATGC AAGAATGGCA	180
TCTCTAAGAG GACTTTTGAA GAAATAAAAG AAGAAATAGC CAGCTGTGGA GATGTTGCTA	240
AAGCAATCAT CAACCTAGCT GTTTATGGTA AAGCCCAGAA CAGATCCTAT GAGCGATTGG	300
CACTTCTGGT TGATACTGTT GGACCCAGAC TGAGTGGCTC CAAGAACCTA GAAAAAGCCA	360
TCCAAATTAT GTACCAAAAC CTGCAGCAAG ATGGGCTGGA GAAAGTTCAC CTGGAGCCAG	420
TGAGAATACC CCACTGGGAG AGGGGAGAAG AATCAGCTGT GATGCTGGAG CCAAGAATTC	480
ATAAGATAGC CATCCTGGGT CTTGGCAGCA GCATTGGGAC TCCTCCAGAA GGCATTACAG	540
CAGAAGTTCT GGTGGTGACC TCTTTGATG AACTGCAGAG AAGGGCCTCA GAAGCAAGAG	600
GGAAGATTGT TGTTTATAAC CAACCTTACA TCAACTACTC AAGGACGGTG CAATACCGAA	660
CGCAGGGGGC GGTGGAAGCT GCCAAGGTGG GGGCTTTGGC ATCTCTCATT CGATCCGTGG	720
CCTCCTTCTC CATCTACAGT CCTCACACAG GTATTCAGGA ATACCAGGAT GGCGTGCCCA	780
AAATTCCAAC AGCCTGTATT ACGGTGGAAG ATGCAGAAAT GATGTCAAGA ATGGCTTCTC	840
ATGGGATCAA AATTGTCATT CAGCTAAAGA TGGGGGCAAA GACCTACCCA GATACTGATT	900
CCTTCAACAC TGTAGCAGAG ATCACTGGGA GCAAATATCC AGAACAGGTT GTACTGGTCA	960
GTGGACATCT GGACAGCTGG GATGTTGGGC AGGGTGCCAT GGATGATGGC GGTGGAGCCT	1020
TTATATCATG GGAAGCACTC TCACTTATTA AAGATCTTGG GCTGCGTCCA AAGAGGACTC	1080

TGCGGCTGGT GCTCTGGACT GCAGAAGAAC AAGGTGGAGT TGGTGCCTTC CAGTATTATC 1140  
 AGTTACACAA GGTAATATT TCCAACCTACA GTCTGGTGAT GGAGTCTGAC GCAGGAACCT 1200  
 TCTTACCCAC TGGGCTGCAA TTTACTGGCA GTGAAAAGGC CAGGGCCATC ATGGAGGAGG 1260  
 TTATGAGCCT GCTGCAGCCC CTCAATATCA CTCAGGTCCT GAGCCATGGA GAAGGGACAG 1320  
 ACATCAACTT TTGGATCCAA GCTGGAGTGC CTGGAGCCAG TCTACTTGAT GACTTATACA 1380  
 AGTATTTCTT CTTCCATCAC TCCCACGGAG ACACCATGAC TGTCATGGAT CCAAAGCAGA 1440  
 TGAATGTTGC TGCTGCTGTT TGGGCTGTTG TTTCTTATGT TGTTGCAGAC ATGGAAGAAA 1500  
 TGCTGCCTAG GTCCTAGAAA CAGTAAGAAA GAAACGTTTT CATGCTTCTG GCCAGGAATC 1560  
 CTGGGTCTGC AACTTTGGAA AACTCCTCTT CACATAACAA TTTCATCCAA TTCATCTTCA 1620  
 AAGCACAACCT CTATTTTCATG CTTTCTGTTA TTATCTTTCT TGATACTTTC CAAATTCCTCT 1680  
 GATTCTAGAA AAAGGAATCA TTCTCCCCTC CCTCCCACCA CATAGAATCA ACATATGGTA 1740  
 GGGATTACAG TGGGGGCATT TCTTTATATC ACCTCTTAAA AACATTGTTT CCACTTTAAA 1800  
 AGTAAACACT TAATAAATTT TTGGAAGATC TCTGAAAAAA AAAAAAAAAA A 1851

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met Lys Phe Leu Ile Phe Ala Phe Phe Gly Gly Val His Leu Leu Ser  
 1 5 10 15  
 Leu Cys Ser Gly Lys Ala Ile Cys Lys Asn Gly Ile Ser Lys Arg Thr  
 20 25 30  
 Phe Glu Glu Ile Lys Glu Glu Ile Ala Ser Cys Gly Asp Val Ala Lys  
 35 40 45  
 Ala Ile Ile Asn Leu Ala Val Tyr Gly Lys Ala Gln Asn Arg Ser Tyr  
 50 55 60  
 Glu Arg Leu Ala Leu Leu Val Asp Thr Val Gly Pro Arg Leu Ser Gly  
 65 70 75 80  
 Ser Lys Asn Leu Glu Lys Ala Ile Gln Ile Met Tyr Gln Asn Leu Gln  
 85 90 95

Gln	Asp	Gly	Leu	Glu	Lys	Val	His	Leu	Glu	Pro	Val	Arg	Ile	Pro	His
Trp	Glu	Arg	Gly	Glu	Glu	Ser	Ala	Val	Met	Leu	Glu	Pro	Arg	Ile	His
Lys	Ile	Ala	Ile	Leu	Gly	Leu	Gly	Ser	Ser	Ile	Gly	Thr	Pro	Pro	Glu
Gly	Ile	Thr	Ala	Glu	Val	Leu	Val	Val	Thr	Ser	Phe	Asp	Glu	Leu	Gln
Arg	Arg	Ala	Ser	Glu	Ala	Arg	Gly	Lys	Ile	Val	Val	Tyr	Asn	Gln	Pro
Tyr	Ile	Asn	Tyr	Ser	Arg	Thr	Val	Gln	Tyr	Arg	Thr	Gln	Gly	Ala	Val
Glu	Ala	Ala	Lys	Val	Gly	Ala	Leu	Ala	Ser	Leu	Ile	Arg	Ser	Val	Ala
Ser	Phe	Ser	Ile	Tyr	Ser	Pro	His	Thr	Gly	Ile	Gln	Glu	Tyr	Gln	Asp
Gly	Val	Pro	Lys	Ile	Pro	Thr	Ala	Cys	Ile	Thr	Val	Glu	Asp	Ala	Glu
Met	Met	Ser	Arg	Met	Ala	Ser	His	Gly	Ile	Lys	Ile	Val	Ile	Gln	Leu
Lys	Met	Gly	Ala	Lys	Thr	Tyr	Pro	Asp	Thr	Asp	Ser	Phe	Asn	Thr	Val
Ala	Glu	Ile	Thr	Gly	Ser	Lys	Tyr	Pro	Glu	Gln	Val	Val	Leu	Val	Ser
Gly	His	Leu	Asp	Ser	Trp	Asp	Val	Gly	Gln	Gly	Ala	Met	Asp	Asp	Gly
Gly	Gly	Ala	Phe	Ile	Ser	Trp	Glu	Ala	Leu	Ser	Leu	Ile	Lys	Asp	Leu
Gly	Leu	Arg	Pro	Lys	Arg	Thr	Leu	Arg	Leu	Val	Leu	Trp	Thr	Ala	Glu
Glu	Gln	Gly	Gly	Val	Gly	Ala	Phe	Gln	Tyr	Tyr	Gln	Leu	His	Lys	Val
Asn	Ile	Ser	Asn	Tyr	Ser	Leu	Val	Met	Glu	Ser	Asp	Ala	Gly	Thr	Phe
Leu	Pro	Thr	Gly	Leu	Gln	Phe	Thr	Gly	Ser	Glu	Lys	Ala	Arg	Ala	Ile
Met	Glu	Glu	Val	Met	Ser	Leu	Leu	Gln	Pro	Leu	Asn	Ile	Thr	Gln	Val
Leu	Ser	His	Gly	Glu	Gly	Thr	Asp	Ile	Asn	Phe	Trp	Ile	Gln	Ala	Gly

405	410	415
Val Pro Gly Ala Ser Leu Leu Asp Asp Leu Tyr Lys Tyr Phe Phe Phe		
420	425	430
His His Ser His Gly Asp Thr Met Thr Val Met Asp Pro Lys Gln Met		
435	440	445
Asn Val Ala Ala Ala Val Trp Ala Val Val Ser Tyr Val Val Ala Asp		
450	455	460
Met Glu Glu Met Leu Pro Arg Ser		
465	470	

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1076 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

CAGAAGTTCA AGGGCCCCCG GCCTCCTGCG CTCCTGCCGC CGGGACCCTC GACCTCCTCA	60
GAGCAGCCGG CTGCCGCCCC GGGAAGATGG CGAGGAGGAG CCGCCACCGC CTCCTCCTGC	120
TGCTGCTGCG CTACCTGGTG GTCGCCCTGG GCTATCATAA GGCCTATGGG TTTTCTGCCC	180
CAAAAGACCA ACAAGTAGTC ACAGCAGTAG AGTACCAAGA GGCTATTTTA GCCTGCAAAA	240
CCCCAAAGAA GACTGTTTCC TCCAGATTAG AGTGGAAGAA ACTGGGTCGG AGTGTCTCCT	300
TTGTCTACTA TCAACAGACT CTTCAAGGTG ATTTTAAAAA TCGAGCTGAG ATGATAGATT	360
TCAATATCCG GATCAAAAAT GTGACAAGAA GTGATGCGGG GAAATATCGT TGTGAAGTTA	420
GTGCCCCATC TGAGCAAGGC CAAAACCTGG AAGAGGATAC AGTCACTCTG GAAGTATTAG	480
TGGCTCCAGC AGTTCCATCA TGTGAAGTAC CCTCTTCTGC TCTGAGTGGA ACTGTGGTAG	540
AGCTACGATG TCAAGACAAA GAAGGGAATC CAGCTCCTGA ATACACATGG TTTAAGGATG	600
GCATCCGTTT GCTAGAAAAT CCCAGACTTG GCTCCCAAAG CACCAACAGC TCATACACAA	660
TGAATACAAA AACTGGAAC TCGCAATTTA ATACTGTTTC CAAACTGGAC ACTGGAGAAT	720
ATTCCTGTGA AGCCCGCAAT TCTGTTGGAT ATCGCAGGTG TCCTGGGAAA CGAATGCAAG	780
TAGATGATCT CAACATAAGT GGCATCATAG CAGCCGTAGT AGTTGTGGCC TTAGTGATTT	840
CCGTTTGTGG CCTTGGTGTA TGCTATGCTC AGAGGAAAGG CTACTTTTCA AAAGAAACCT	900



CCTTCCAGAA GAGTAATTCT TCATCTAAAG CCACGACAAT GAGTGAAAAT GATTTC AAGC 960  
 ACACAAAATC CTTTATAATT TAAAGACTCC ACTTTAGAGA TACACCAAAG CCACCGTTGT 1020  
 TACACAAGTT ATTAAACTAT TATAAAACTC AAAAAAAAAA AAAAAAAAAA AAAAAA 1076

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Met	Ala	Arg	Arg	Ser	Arg	His	Arg	Leu	Leu	Leu	Leu	Leu	Leu	Arg	Tyr	1	5	10	15
Leu	Val	Val	Ala	Leu	Gly	Tyr	His	Lys	Ala	Tyr	Gly	Phe	Ser	Ala	Pro	20	25	30	
Lys	Asp	Gln	Gln	Val	Val	Thr	Ala	Val	Glu	Tyr	Gln	Glu	Ala	Ile	Leu	35	40	45	
Ala	Cys	Lys	Thr	Pro	Lys	Lys	Thr	Val	Ser	Ser	Arg	Leu	Glu	Trp	Lys	50	55	60	
Lys	Leu	Gly	Arg	Ser	Val	Ser	Phe	Val	Tyr	Tyr	Gln	Gln	Thr	Leu	Gln	65	70	75	80
Gly	Asp	Phe	Lys	Asn	Arg	Ala	Glu	Met	Ile	Asp	Phe	Asn	Ile	Arg	Ile	85	90	95	
Lys	Asn	Val	Thr	Arg	Ser	Asp	Ala	Gly	Lys	Tyr	Arg	Cys	Glu	Val	Ser	100	105	110	
Ala	Pro	Ser	Glu	Gln	Gly	Gln	Asn	Leu	Glu	Glu	Asp	Thr	Val	Thr	Leu	115	120	125	
Glu	Val	Leu	Val	Ala	Pro	Ala	Val	Pro	Ser	Cys	Glu	Val	Pro	Ser	Ser	130	135	140	
Ala	Leu	Ser	Gly	Thr	Val	Val	Glu	Leu	Arg	Cys	Gln	Asp	Lys	Glu	Gly	145	150	155	160
Asn	Pro	Ala	Pro	Glu	Tyr	Thr	Trp	Phe	Lys	Asp	Gly	Ile	Arg	Leu	Leu	165	170	175	
Glu	Asn	Pro	Arg	Leu	Gly	Ser	Gln	Ser	Thr	Asn	Ser	Ser	Tyr	Thr	Met	180	185	190	
Asn	Thr	Lys	Thr	Gly	Thr	Leu	Gln	Phe	Asn	Thr	Val	Ser	Lys	Leu	Asp				

195	200	205
Thr Gly Glu Tyr Ser Cys Glu Ala Arg Asn Ser Val Gly Tyr Arg Arg		
210	215	220
Cys Pro Gly Lys Arg Met Gln Val Asp Asp Leu Asn Ile Ser Gly Ile		
225	230	235 240
Ile Ala Ala Val Val Val Val Ala Leu Val Ile Ser Val Cys Gly Leu		
	245	250 255
Gly Val Cys Tyr Ala Gln Arg Lys Gly Tyr Phe Ser Lys Glu Thr Ser		
	260	265 270
Phe Gln Lys Ser Asn Ser Ser Ser Lys Ala Thr Thr Met Ser Glu Asn		
	275	280 285
Asp Phe Lys His Thr Lys Ser Phe Ile Ile		
290	295	

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2522 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GAAAGGTTGT GTAGCTTGCC CTGGTTGCAT AGTTAAACGA GGGCTAGAAA CAGGACTAGG	60
AGTCAGGCCT GTCCAGCTGG AAAACTTGGG TTTTCTAGAA GGGGTACCCT GGCCTCCTGC	120
GGAGCCTGCT GTGGGACTCT GCAGAACACA ATTCAAGGCC AGACTGAACA CTAGCCTGAA	180
CCTGCCCTGA GAATCCCTCT AAGCCGACCT ACTCCACAGC TGTCCTGACT GTGTAAGCGA	240
GATGATGATT AGTGATCAGA CGAAAGGATT CCTGTGATTG GTAACCTCT CAAAGTATTT	300
GGAAAACAGT TCAATTTTCA TCTATTTTCA AAGCACGCCG TGGTGTCTAT TGAGGCTCAC	360
CTGCATTGAA TTCCTTCCTT TTTATGTTGC GATCTCCCAA GATTGCATTG TGGAGTGTTT	420
TCGAATCCAT TTTGAAATCC CCGTGCGTGC GCTATGCAGG CCTCAGTCTT TTTCCATTCC	480
ATTCTTAACT CTACTTTCGA CGGAAGCAGT GTTTTACCCC GAACTGGCT TGCCTAGGAC	540
CTTGTGCTCT GCACAACTAG CAGGGCCCGG CAGGATGTAC TGAATTCTTG CTCTCGTGTC	600
CAGCTGGACG GTGATGGCTT TCAAGTCCTT GGCTGTTGGG AGCTTACTAT AAATGTTTCGT	660
CTTGGCTACA AACTCTCCAC TCTTTCCTCG GCACTCTCTC AGCATTGCCA CCACTGTCTT	720

TCCTCTTGGC	CAACTGTTTT	CTTTACTTAG	GCTTTCCCTT	GCTAGAAAGT	CCAGGTAACT	780
TTCTCCACGG	GACCTGGTTT	CCTTCGCACA	TCCCAGCTGG	CCTCGAGGAA	AGGTAGCTCT	840
TCCAAATCAG	AGAATCTGGA	TGCTGGGCTG	GGCTCTGCAC	CAACCAGCTG	GGCCGCTTCA	900
CCCCTGGGGC	CCCAAACACTAC	TCATCTGTGA	AGCGAAGGCA	CCGCGCTTGA	TGCCTTCTGC	960
AACGTTCTTC	AGTTTGGAAA	TCCTTCTGTT	TCGTTGGGGA	TATTTACAGG	CCTCTTCTCA	1020
AGGTTGCACT	TTTGCCAGCT	GCCAGGGATC	GTCTCAAAAC	AGGTTCTTAG	TGCATTCTATA	1080
GCTTGAGCTG	CTGTCTTGAA	AGTAGTACAT	TCCTTTTTCT	GCCAACTTTT	TTCTGAGAAA	1140
GTTTTTGAAT	GCACACGTGC	ACCCAACAGA	GTGAGAGTGG	CTGTAAAGAG	AGAGGGCGCC	1200
ATTTCTTTTG	CCCTCCAGCC	TGTCCCTGTG	CACCCTGGAG	GGGCCCCTTT	TTTCCACCGC	1260
TTAGATAAAA	TCTAGGGCAA	GTTCTGAAC	TTCTCTTGTC	TCTCTCAGGT	AACAAAAATT	1320
CTTTTGGGCT	CCTTTAGTCA	CAAAGATATT	CACGATTTCA	GGTATTAAAG	TGCCCAGCCC	1380
TGGGTGATTG	TCAAAATTCT	GAAGTTGATT	TAAAGTGGCA	CCTCCTCTCA	CAGTCTTCGG	1440
GAGGGAGAGA	CCGGAGCCAG	GAGTGCAGCG	TGTTTGCTGG	GGTCTGTCGT	GGCCCACTCC	1500
ACACCTGCTG	GGTGGATCCG	GCTGGTGCCC	CATGGGCGCC	TCTGAGATGC	CCCTCCCCAC	1560
CCCATCAGTG	GCGCTGTCTC	ACCTGCAGGC	TGTTCTCACA	GGTGGTCCCC	CCTCACTCCT	1620
CCTGCAGCCC	CAGTTCCTGG	CTGTTTATTC	TTATTGGGAC	CCGTCACCCT	CCTGGAGGCG	1680
GTCCCAGCCG	AGCCCCCTTA	AGACAGCACC	AGGCTGGCTC	CACTTGGCCC	CCGCTGGTTC	1740
AGGGAAGTGC	TGCTGCAGCC	GTTTAGTTTG	ACAAAGGAGG	CAGCGAGGCC	GTCTCATTGG	1800
TAGCCCTCTC	CTGGCTTGCC	CAGCCACCAC	CTCACCTCGA	TTCCTCCAG	GCCTGGGTCC	1860
AGCACCAGCC	TAGGAAGAGG	GTGCCCCATG	CTGTCTAGCT	CTTCTTCGGG	ATGGGGGGCT	1920
CCAGGTTCTT	TGGTATTTTG	CTTTGGCCTT	TGGAGCCTCA	GTCAAACTG	AGGAAAGGTG	1980
TCATTTTCAC	ATCTCGTCAC	ACGTACAGTG	ACTGCAACTA	AAAGCACAGG	CTTTGTAGAA	2040
ACAGACATGG	GTTCAGGCCC	CAGCTCCACC	ATTACACAAGG	TGTGTGGCTT	CCTGCAAGGT	2100
ACCTTCATCT	CTGAGTTACC	TGACTCCATC	TGAGTTTCCT	TCTTGTAATA	CTGGCATCCA	2160
TGAAAGTGGC	TACCTCGAAG	GGCGTGAAGA	TGAAATGAGG	TGGAAAGTAG	GTAGCCCCCG	2220
AATGAGGGAA	GCATTGAGTG	AGAGCTGGCC	CTCTGACCCT	TCTAAAAGAA	CACAGCCAAC	2280
TTTTTTAACT	GTCTTTCCAG	AAAGAGATGG	AAAACCTCGA	AGCCCCCTTC	CACTGCCTTG	2340
CCAAGCAGTT	CCACCAGCTG	TACCGGGAGA	AGGTGGAGGT	TTTCCGGGCC	CTGGCATGAC	2400
GAGCTGGAGC	AGATCGTGCT	GCACAACCGG	AGAAGACAGA	ATTACCTCTG	CTCTTTTAAT	2460

ATATAATGAT GGCTTTAAAT AAAATTAGGA GAAAATGTCA AAAAAAAAAA AAAAAAAAAA 2520

AA 2522

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 113 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Met	Met	Ile	Ser	Asp	Gln	Thr	Lys	Gly	Phe	Leu	Ser	Leu	Val	Thr	Leu	
1				5					10					15		
Ser	Lys	Tyr	Leu	Glu	Asn	Ser	Ser	Ile	Phe	Ile	Tyr	Phe	Arg	Ser	Thr	
			20					25					30			
Pro	Trp	Cys	Leu	Leu	Arg	Leu	Thr	Cys	Ile	Glu	Phe	Leu	Pro	Phe	Tyr	
		35					40					45				
Val	Ala	Ile	Ser	Gln	Asp	Cys	Ile	Val	Glu	Cys	Phe	Arg	Ile	His	Phe	
		50				55					60					
Glu	Ile	Pro	Val	Arg	Ala	Leu	Cys	Arg	Pro	Gln	Ser	Phe	Ser	Ile	Pro	
65				70					75					80		
Phe	Leu	Thr	Leu	Leu	Ser	Thr	Glu	Ala	Val	Phe	Tyr	Pro	Asp	Thr	Gly	
			85					90						95		
Leu	Pro	Arg	Thr	Leu	Cys	Ser	Ala	Gln	Leu	Ala	Gly	Pro	Gly	Arg	Met	
			100					105					110			
Tyr																

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1962 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CCCCGGGCCCC	AGCCTTCTCC	AGAACCCCTG	CTACCCACGA	CTAAGCCCCG	AACAATCTGC	60
CCTTGGGCTT	GTTCTCTTCG	CAGTTGTCGG	CCCTGGGCCG	GGAGCTGGAG	TCCCAGACTC	120

ATAGGTCCCG	CCCCAGCCCC	CGAAGAGCCG	CCTCAGCCGG	GGGGAGTTGC	TCGGACTCAA	180
ACGTCCAGTC	CTCGTGCGAC	CGCGCTGGGT	CGGAAGTGAG	CAGGCTGAGG	CCACCATGGA	240
GCAGTGTGCG	TGCGTGAGGA	GAGAGCTGGA	CAAGGTCTCG	CAGAAGTTCC	TGACCTACGG	300
GCAGCACTGT	GAGCGGAGCC	TGGAGGAGCT	GCTGCACTAC	GTGGGCCAGC	TGCGGGCTGA	360
GCTGGCCAGC	GCAGCCCTCC	ARGGGACCCC	TCTCTCAGCC	ACCCTCTCTC	TGGTGATGTC	420
ACAGTGCTGC	CGGAAGATCA	AAGATACGGT	GCAGAACTG	GCTTCGGAMC	ATAAGGACAT	480
TCACAGCAGT	GTATCCCGAG	TGGGCAAAGC	CATTGACAGG	AACTTCGACT	CTGAGATCTG	540
TGGTGTTGTG	TCAGATGCGG	TGTGGGACGC	GCGGGAACAG	CAGCAGCAGA	TCCTGCAGAT	600
GGCCATCGTG	GAACACCTGT	ATCAGCAGGG	CATGCTCAGC	GTGGCCGAGG	AGCTGTGCCA	660
GGAATCAACG	CTGAATGTGG	ACTTGGATTT	CAAGCAGCCT	TTCCTAGAGT	TGAATCGAAT	720
CCTGGAAGCC	CTGCACGAAC	AAGACCTGGG	TCCTGCGTTG	GAATGGGCCG	TCTCCACAG	780
GCAGCGCCTG	CTGGAACTCA	ACAGCTCCCT	GGAGTTCAAG	CTGCACCGAC	TGCACTTCAT	840
CCGCCCTTTG	GCAGGAGGCC	CCGCGAAGCA	GCTGGAGGCC	CTCAGCTATG	CTCGGCACTT	900
CCAGCCCTTT	GCTCGGCTGC	ACCAGCGGGA	GATCCAGGTG	ATGATGGGCA	GCCTGGTGTA	960
CCTGCGGCTG	GGCTTGAGGA	AGTCACCCTA	CTGCCACCTG	CTGGACAGCA	GCCACTGGGC	1020
AGAGATCTGT	GAGACCTTTA	CCCGGGACGC	CTGTTCCCTG	CTGGGGCTTT	CTGTGGAGTC	1080
CCCCCTTAGC	GTCAGCTTTG	CCTYTGGCTG	TGTGGCGCTG	CCTGTGTTGA	TGAACATCAA	1140
GGCTGTGATT	GAGCAGCGGC	AGTGCCTGG	GGTCTGGAAT	CACAAGGACG	AGTTACCGAT	1200
GAGATTGAAC	TAGGCATGAA	GTGCTGGTAC	CACTCCGTGT	TCGCTTGCCC	CATCCTCCGC	1260
CAGCAGACGT	CAGATTCCAA	CCCTCCCATC	AAGCTCATCT	GTGGCCATGT	TATCTCCCGA	1320
GATGCACTCA	ATAAGCTCAT	TAATGGAGGA	AAGCTGAAGT	GTCCCTACTG	TCCCATGGAG	1380
CAGAACCCGG	CAGATGGGAA	ACGCATCATA	TTCTGATTCC	TACCTGGAAG	GAATTTTGTT	1440
GAAAGGGGTT	TTCACCTGTG	AGCCTTGGTC	TGTCTCGGTA	GGGTGGTCAA	CTTCAGTGGA	1500
CTGTGGTTGG	TTTCAGAGCG	CCTGGCTGAG	GAGTTCCACT	GAGGGGAGCA	CTGGAGCAGC	1560
CCTTTGGCAG	AGGCTGAGGA	GGGAGATGGA	CCAGCCCACG	CCTGGCACCT	GGCTCCATGG	1620
CATAAGGAAA	GGGAGATGCT	GGCCTCTGTG	CTCCTGCTGT	CTTTTCCTGT	TTCTGTTTGC	1680
GTTTGACTTA	GTAGCAACCG	ACAGAGTGGC	AAGGGATTGT	GTCTTCAGCA	GTAGACATCC	1740
TTCCACCCCT	GCCCTCAGCC	AAGTCTCTTG	CTGCCATGCC	AATGCTATGT	CCACCCCTTG	1800

CCCTCGGCCC AAGAGTGTCC AGCGGTGGCC CACYTYTTCC TCCCACTACA GCCTCAACAG 1860  
TATGTACCAT CTCCCACTGT AAATAGTCCC AGTTAGAACG GAATGCCGTT GTTTTATAAC 1920  
TTTGAACAAA TGTATTTACT GCCAAAAAAA AAAAAAAAAA AA 1962

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Met	Glu	Gln	Cys	Ala	Cys	Val	Glu	Arg	Glu	Leu	Asp	Lys	Val	Leu	Gln	1	5	10	15
Lys	Phe	Leu	Thr	Tyr	Gly	Gln	His	Cys	Glu	Arg	Ser	Leu	Glu	Glu	Leu	20	25	30	
Leu	His	Tyr	Val	Gly	Gln	Leu	Arg	Ala	Glu	Leu	Ala	Ser	Ala	Ala	Leu	35	40	45	
Gln	Gly	Thr	Pro	Leu	Ser	Ala	Thr	Leu	Ser	Leu	Val	Met	Ser	Gln	Cys	50	55	60	
Cys	Arg	Lys	Ile	Lys	Asp	Thr	Val	Gln	Lys	Leu	Ala	Ser	Xaa	His	Lys	65	70	75	80
Asp	Ile	His	Ser	Ser	Val	Ser	Arg	Val	Gly	Lys	Ala	Ile	Asp	Arg	Asn	85	90	95	
Phe	Asp	Ser	Glu	Ile	Cys	Gly	Val	Val	Ser	Asp	Ala	Val	Trp	Asp	Ala	100	105	110	
Arg	Glu	Gln	Gln	Gln	Gln	Ile	Leu	Gln	Met	Ala	Ile	Val	Glu	His	Leu	115	120	125	
Tyr	Gln	Gln	Gly	Met	Leu	Ser	Val	Ala	Glu	Glu	Leu	Cys	Gln	Glu	Ser	130	135	140	
Thr	Leu	Asn	Val	Asp	Leu	Asp	Phe	Lys	Gln	Pro	Phe	Leu	Glu	Leu	Asn	145	150	155	160
Arg	Ile	Leu	Glu	Ala	Leu	His	Glu	Gln	Asp	Leu	Gly	Pro	Ala	Leu	Glu	165	170	175	
Trp	Ala	Val	Ser	His	Arg	Gln	Arg	Leu	Leu	Glu	Leu	Asn	Ser	Ser	Leu	180	185	190	
Glu	Phe	Lys	Leu	His	Arg	Leu	His	Phe	Ile	Arg	Leu	Leu	Ala	Gly	Gly	195	200	205	

Pro Ala Lys Gln Leu Glu Ala Leu Ser Tyr Ala Arg His Phe Gln Pro  
 210 215 220  
 Phe Ala Arg Leu His Gln Arg Glu Ile Gln Val Met Met Gly Ser Leu  
 225 230 235 240  
 Val Tyr Leu Arg Leu Gly Leu Glu Lys Ser Pro Tyr Cys His Leu Leu  
 245 250 255  
 Asp Ser Ser His Trp Ala Glu Ile Cys Glu Thr Phe Thr Arg Asp Ala  
 260 265 270  
 Cys Ser Leu Leu Gly Leu Ser Val Glu Ser Pro Leu Ser Val Ser Phe  
 275 280 285  
 Ala Xaa Gly Cys Val Ala Leu Pro Val Leu Met Asn Ile Lys Ala Val  
 290 295 300  
 Ile Glu Gln Arg Gln Cys Thr Gly Val Trp Asn His Lys Asp Glu Leu  
 305 310 315 320  
 Pro Met Arg Leu Asn  
 325

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 745 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

AAAAACACAA AACCCCGTAA AATCACAAAG AAAATCCAAC ACCAAAGGCG CAGAAGCCGG 60  
 CTGGCCGTGG TGGGGGCAGC GTAGGCGTAG CATCCCTCTC CTCTCACTTA GCCTGTTGAC 120  
 TCTTGTTATT ATCATGATAT TCACAAAACG CCGCATGTTT AAAAAGTCAT AGATGTCATC 180  
 TTCTCTCTGC CCCAGGGAG GAAAGCCACC TTCTCTTGCC CCTTGGCCCC TTTGTCAGGG 240  
 GCCAGGGGTC TGCCGGGTGG GGGTGCCAAC AGGCCTGGCC CTTTCCTCCC CTGCATCCAG 300  
 CCATGGGGGC CTCTGCGATT GCCGGAAGGT TGCATGGCTG GTCCCAGGGC CAGCACAGGC 360  
 CCGAGGCCGG GCTGCCTGGT TTTATTTTTA TTAACTTTA TTTTCTGTTT TATGAGTGTG 420  
 TGTCCGCCCA CCCCCACCCC CTTCACTGTT AAGTGGGGAG CCCTGGGGGA GTCTCTCCTG 480  
 CCTCCCAGCC TCTCCAAGA CCTCCCCCT CGTCACCAGC CATCCCTCTG GACCAGGCAG 540

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AGGGCGGACC GGGTGGGCAG GGGCCTGAGG GTGGCTCGGG CCAGCCCACC AGCCAATGGA      600
CCCCTCCTCA GGCCGCCAGT GTCGCCCTGC CCCTTTTAA AACAAAATGC CCTCGTTTGT      660
AAACCCTTAG ACGCTTGAGA ATAAACCCCT TCCTTTTCTT CCAAAAAAAAA AAAAAAAAAA      720
AAAAAAAAAA AAAAAAAAAA AAAAAA                                           745

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(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 114 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

```

Met Ala Gly Pro Arg Ala Ser Thr Gly Pro Arg Pro Gly Cys Leu Val
1              5              10              15

Leu Phe Leu Phe Asn Phe Ile Phe Cys Phe Met Ser Val Cys Pro Pro
              20              25              30

Thr Pro Thr Pro Phe Ser Val Lys Trp Gly Ala Leu Gly Glu Ser Leu
35              40              45

Leu Pro Pro Ser Leu Ser Gln Asp Leu Pro Pro Arg His Gln Pro Ser
50              55              60

Leu Trp Thr Arg Gln Arg Ala Asp Arg Val Gly Arg Gly Leu Arg Val
65              70              75              80

Ala Arg Ala Ser Pro Pro Ala Asn Gly Pro Leu Leu Arg Pro Pro Val
85              90              95

Ser Pro Cys Pro Phe Leu Lys Gln Asn Ala Leu Val Cys Lys Pro Leu
100             105             110

Asp Ala

```

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1983 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TGGCAATAGT GGTTAGGGAA GGCTCCTTTG AGGAAGTGAA TTTT TAGCTG AGACTTAAAG 60  
AACAAATGAG ATTTAGCTAG AAAAATTGGA CATGCGATGC CAAGATGGCA TTTTAAAAGA 120  
ATAATAGTAA GCACAAAGGC CCTGTAGCAG GAGGGAGCTG ATTGTCCATA GTTCAGACAG 180  
CAAAGAAGCT GATGATGCAG GTTGGGGTCA GACCGTGTTT GACTACAGAT AGGATGTTAA 240  
GGGTTTGGC TTTT TAGGTT TTTGTTTAA TTCTAAAAGT AATGGAAAAT GTACTCCTTT 300  
TGGTGGTGGT CTGAGAGAAG GTACATCATT AGAATGACAT TTTGAAAACA AACTCAGGC 360  
TGCTCAGTAG AGAATGGCTT CAAAGGATTT AAAAGCAGAA GCAGAAGGAC ATATTAGAGA 420  
AGGATTGTAT AGTTTCTGG TAAAAGATGA CAGTGAATTG TATGGGCGAT GGATTAGCCG 480  
TGGAAGGTGT TGAGTATAAG TGGTCTCCAG CCAA CTCTA TGGTTACTGG AATAAGAGAG 540  
TAGGAACCTT TCTCAGGCTT TATCTTTATC TATTCTTGTC AACAGTATGT ACATGTGTCC 600  
CCCAGCCCCA AATACTGTA CAGTTTAATG ATGTTCACTC TATACAGTTC CCAGAATCCA 660  
TTGGAAATTG CTGTAACAGC ATATCCTCAA TGCCCATCAA TTCTCCACGT CCAACTTCTC 720  
CATGGCCTCC TCTGCCTCTG CTGATCTGTG AACTTCCCAA GCCCCTTCCC CTACCTGCTT 780  
TTGATTGGCT TTAAC TTTTA CAATATCTTC ATTACTCCAA GTTTGTTCAA CATCCTTTTT 840  
ATTTTTTTAA ATCATAGATT GATTTAGTTT ATTCTCTTTG CCATTTTTGA ATCTCATTAT 900  
TTCTGTTTCT CCTTGGTTAT TAGTGGCTCT GTTTTCCTTC AATTGCCTCT TGTCTTTGAG 960  
AAGCTCTTGT GATTCTTTTA GGGCCATTTG CCATTGATT GGTGTGTCTT CCTTTTCCCT 1020  
ATAAGCTTTA AATATGGCAT TATAGTTTTA TCCCCTTTCC TCTTCTTTAG GTACAACTGC 1080  
AGACACTTTG CTCTCCAAG GTTACTAAGC AGTGTCTGAC ACAATGTAGA AGCTCAACAA 1140  
ATATTGGTTA AATTTATTTT TTCTATTGAT TGTTCAGGCT TTGATGACAT CACTTAAAT 1200  
GTTTCTTGTA CACACCCTGT TTTCTACTGA TATATGTATG TGTATGGCTA CCTGAATCCA 1260  
GGTTTCTTCT AGGAATATAC AGAAAGTAAT TGATTCTCT GTGGATCTCT AACAGTGACA 1320  
AGAATTTTCA CCTATGCCTG TGAGAATACC TTCAAAAGTA TTGGGTGCTC ATCATAAACA 1380  
CACATCAGTT TAACAACTC TTATGGATGC ATTGACTTTC CCAGTTAGTT GCTAGATGAC 1440  
TTCGGATGAT TTGCATAATG GGTCTCAGTT TCCATATCTG TTAAATGGCA ATAATCAGAG 1500  
AATTTTAAAA AATTTAAGGA CACCTGGAAA GCTTGAAAGA TCCCTAGAAA GCATGTGTTT 1560  
ATTCCACATA GTGGGAACTA TGCTAGATT CCAAAGACAC AAAGACAACT AAGACAACTT 1620

AGAATAAGAA GGAAAAGAGA ATGATTCGTT GCAATGATCC CCTTGAAGCT CCAGTTGAAA 1680  
 GTCAGAGTAT TGCCCTGGAT TGGAAGTAGT CTCCAAACTG ACATCATTTT CTTTTTCGAA 1740  
 CCATATCTGG CCTGTCTCTC TTGCCAGTTG CATATTAAAG GTAACAGATT TGAAAATGTT 1800  
 TGGAATAAAA GCTCTAGTTA GGTGTGGTGG CACACACCTG CCATCCCAGC TACTGGAGAG 1860  
 TCTGAGACTC GATGATTGTT TCAGCCCAAG AGTTGGAGGT TGTAGTGAGC TATGATGGCA 1920  
 CCACTGCACT CCAGTCTGTG TGACAGAGCG AAGACCTTGT CTCTAAGGAA AAAAAAAAAA 1980  
 AAA 1983

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Met Thr Val Asn Cys Met Gly Asp Gly Leu Ala Val Glu Gly Val Glu  
 1 5 10 15  
 Tyr Lys Trp Ser Pro Ala Lys Leu Tyr Gly Tyr Trp Asn Lys Arg Val  
 20 25 30  
 Gly Thr Leu Leu Arg Leu Tyr Leu Tyr Leu Phe Leu Ser Thr Val Cys  
 35 40 45  
 Thr Cys Val Pro Gln Pro Gln Ile Thr Val Gln Phe Asn Asp Val His  
 50 55 60  
 Ser Ile Gln Phe Pro Glu Ser Ile Gly Asn Cys Cys Asn Ser Ile Ser  
 65 70 75 80  
 Ser Met Pro Ile Asn Ser Pro Arg Pro Thr Ser Pro Trp Pro Pro Leu  
 85 90 95  
 Pro Leu Leu Ile Cys Glu Leu Pro Lys Pro Leu Pro Leu Pro Ala Phe  
 100 105 110  
 Asp Trp Leu  
 115

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1046 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GGGCTTAGTT AGGAGCTATG GCTAAACATC ATCCTGATTT GATCTTTTGC CGCAAGCAGG	60
CTGGTGTGTC CATCGGAAGA CTGTGTGAAA AATGTGATGG CAAGTGTGTG ATTTGTGACT	120
CCTATGTGCG TCCCTGCACT CTGGTGCGCA TATGTGATGA GTGTAACATAT GGATCTTACC	180
AGGGGCGCTG TGTGATCTGT GGAGGACCTG GGGTCTCTGA TGCCTATTAT TGTAAGGAGT	240
GCACCATCCA GGAGAAGGAC AGAGATGGCT GCCCAAAGAT TGTCAATCTG GGGAGCTCTA	300
AGACAGACCT CTTCTATGAA CGCAAAAAAT ACGGCTTCAA GAAGARGTGA TTGGTGGGTG	360
GCCCCCTCCT CCCCCCAACA TCAGTCTGCT GCAGCTGCCA GAAAACATGC CTACTACTAC	420
CAGCAGAAAG GGAGCAGAGC CCAGAGCATC ACCAGGAGTG CCTGCTAGTG TACTGGCAGC	480
TTGCCACCCC CTCCTCTCCC TTCACCCAGA CACGTGGTAG GGATGGAAAA GGATTCTTCA	540
CAGAGCACTC TGGCACACCA TATCGGAGAA AACTTGATAG ATTAGTTAAT GGTTTTTCTT	600
GAATTCGAGA AGCATAGATC TGTTCCTCAT ATTGGTATGT TCTCCCTCAA CCAAGATCTT	660
CTAAAAAGAA ATAATATTTT AGTCTTCTGC TTGAGGAACT GACTGTGAAG CGACGCCCAG	720
TGAAAAACAT GTTCTTGCA GAGCTCTGGT GGCAGCTGTC CTTGAGGAAC CTTTGGTGTG	780
TGGTGGGAAG CTATCAGAAC AAGAAATGTA GGCATTTCCC GTTTTTTTGG GGGGGGGGGG	840
TGGGGGGGCA GGGCTCTGCC CTCTTGAAAG GCATTTACTT GTTTAACTACT TGTCCAGCTA	900
CAGTGGGGTA CAGTAGCTGG CTATTCACAG GCATCATCAT AGCCCACTAG TCTCATATTA	960
TTTTCCTTTT GAGAAATTGG AACTCTTTC TGTGCTATT ATATTAATAA AGTTGGTGTT	1020
TATTTTCTGG TAAAAAAAAA AAAAAA	1046

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 110 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Met	Ala	Lys	His	His	Pro	Asp	Leu	Ile	Phe	Cys	Arg	Lys	Gln	Ala	Gly	
1				5					10					15		
Val	Ala	Ile	Gly	Arg	Leu	Cys	Glu	Lys	Cys	Asp	Gly	Lys	Cys	Val	Ile	
			20					25					30			
Cys	Asp	Ser	Tyr	Val	Arg	Pro	Cys	Thr	Leu	Val	Arg	Ile	Cys	Asp	Glu	
		35					40					45				
Cys	Asn	Tyr	Gly	Ser	Tyr	Gln	Gly	Arg	Cys	Val	Ile	Cys	Gly	Gly	Pro	
	50					55					60					
Gly	Val	Ser	Asp	Ala	Tyr	Tyr	Cys	Lys	Glu	Cys	Thr	Ile	Gln	Glu	Lys	
65					70					75					80	
Asp	Arg	Asp	Gly	Cys	Pro	Lys	Ile	Val	Asn	Leu	Gly	Ser	Ser	Lys	Thr	
				85					90					95		
Asp	Leu	Phe	Tyr	Glu	Arg	Lys	Lys	Tyr	Gly	Phe	Lys	Lys	Xaa			
			100					105					110			

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1814 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

ATCTTGCAGT	GGGCCTCTGT	CCCAAAAACA	AGCAGAATTT	TTTCTTTCTC	AACAGGCTTC	60
TTTGCTAAAG	AATGATGAGA	CTAAGGCCCT	CACTCCAGCT	TCCTTGCAGA	AGGAATTAAA	120
CAATTTGTTG	AAATTTAATC	CTGATTTTGC	TGAAGCGCAT	TATCTCAGCT	ACTTAAACAA	180
CCTCCGTGTC	CAAGATGTTT	TCAGTTCAAC	ACACAGTCTC	CTCCATTATT	TTGATCGTCT	240
GATTCTTACC	GGAGCCGAAA	GCAAAAGTAA	TGGGGAAGAR	GGCTATGGCC	GGAGCTTGAG	300
ATACGCCGCT	CTGAATCTTG	CCGCCCTGCA	CTGCCGCTTC	GGTCACTATC	AACAGGCAGA	360
GCTCGCCCTG	CAGGARGCAA	TTAGGATTGC	CCAGGARTCC	AACGATCACG	TGTGTCTCCA	420
GCACTGTTTG	AGCTGGCTTT	ATGTGCTGGG	GCAGAAGAGA	TCCGATAGCT	ATGTTCTGCT	480
GGAGCATTCT	GTGAAGAAGG	CAGTACATTT	TGGGTTACCG	TACCTCGCCT	CCCTGGGAAT	540
ACAGTCCCTT	GTTCAACAGA	GAGCTTTTGC	TGGGAAGACG	GCAAACAAGC	TGATGGATGC	600

CCTAAAGGAC TCCGACYTCC TGCACTGGAA ACACAGCCTG TCAGAGCTCA TCGATATCAG	660
CATCGCACAG AAAACGGCCA TCTGGAGGCT GTATGGCCGC AGCACCATGG CACTGCAACA	720
GGCCCAGATG TTGCTGAGCA TGAACAGCCT GGAGGCGGTG AATGCGGGCG TGCAGCAGAA	780
CAACACAGAG TCCTTTGCTG TCGCACTCTG CCACCTCGCA GAGCTACACG CGGAGCAGGG	840
CTGTTTTGCT GCAGCTTCTG AAGTGTTAAA GCACTTGAAG GAACGATTTT CGCCTAATAG	900
TCAGCACGCC CAGTTATGGA TGCTATGTGA TCAAAAAATA CAGTTTGACA GAGCAATGAA	960
TGATGGCAAA TATCATTTGG CTGATTCCTT TGTTACAGGA ATCACAGCTC TCAATAGCAT	1020
AGAGGGTGTT TATAGGAAAG CGGTTGTATT ACAAGCTCAG AACCAAATGT CAGAGGCACA	1080
TAAGCTTTTA CAAAAATTGT TGGTTCATTG TCAGAACTG AAGAACACAG AAATGGTGAT	1140
CAGTGTCCTA CTGTCCGTGG CAGAGCTGTA CTGGCGATCT TCCTCCCCTA CCATCGCGCT	1200
GCCCATGCTC CTGCAGGCTC TGGCCCTCTC CAAGGAGTAC CGGTTACAGT ACTTGGCCTC	1260
TGAAACAGTG CTGAACTTGG CTTTTGCGCA GCTCATTCTT GGAATCCCAG AACAGGCCTT	1320
AAGTCTTCTC CACATGGCCA TCGAGCCCAT CTTGGCTGAC GGGGCTATCC TGGACAAAGG	1380
TCGTGCCATG TTCTTAGTGG CCAAGTGCCA GGTGGCTTCA GCAGCTTCCT ACGATCAGCC	1440
GAAGAAAGCA GAAGCTCTGG AGGCTGCCAT CGAGAACCTC AATGAAGCCA AGAACTATTT	1500
TGCAAAGGTT GACTGCAAAG AGCGCATCAG GGACGTCGTT TACTTCCAGG CCAGACTCTA	1560
CCATACCCTG GGGAAGACCC AGGAGAGGAA CCGGTGTGCG ATGCTCTTCC GGCAGCTGCA	1620
TCAGGAGCTG CCCTCTCATG GGGTACCCTT GATAAACCAT CTCTAGAGAG GACATCCCTG	1680
CTGGGCTGCT GTGCAGAGTA TAAGATTTTG GACTTGTTCA TGTCCCCTCT CTCCCTATAA	1740
ATGATGTATT TGTGACACCC TATCTTGTC AATAACAGCA TTCTGATTAG TTTGTCTTAA	1800
AAAAAAAAAA AAAA	1814

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Met Asp Ala Leu Lys Asp Ser Asp Xaa Leu His Trp Lys His Ser Leu

1		5		10		15									
Ser	Glu	Leu	Ile	Asp	Ile	Ser	Ile	Ala	Gln	Lys	Thr	Ala	Ile	Trp	Arg
		20						25					30		
Leu	Tyr	Gly	Arg	Ser	Thr	Met	Ala	Leu	Gln	Gln	Ala	Gln	Met	Leu	Leu
		35					40					45			
Ser	Met	Asn	Ser	Leu	Glu	Ala	Val	Asn	Ala	Gly	Val	Gln	Gln	Asn	Asn
	50					55					60				
Thr	Glu	Ser	Phe	Ala	Val	Ala	Leu	Cys	His	Leu	Ala	Glu	Leu	His	Ala
65					70					75					80
Glu	Gln	Gly	Cys	Phe	Ala	Ala	Ala	Ser	Glu	Val	Leu	Lys	His	Leu	Lys
				85					90					95	
Glu	Arg	Phe	Pro	Pro	Asn	Ser	Gln	His	Ala	Gln	Leu	Trp	Met	Leu	Cys
			100					105					110		
Asp	Gln	Lys	Ile	Gln	Phe	Asp	Arg	Ala	Met	Asn	Asp	Gly	Lys	Tyr	His
		115					120					125			
Leu	Ala	Asp	Ser	Leu	Val	Thr	Gly	Ile	Thr	Ala	Leu	Asn	Ser	Ile	Glu
	130					135					140				
Gly	Val	Tyr	Arg	Lys	Ala	Val	Val	Leu	Gln	Ala	Gln	Asn	Gln	Met	Ser
145					150					155					160
Glu	Ala	His	Lys	Leu	Leu	Gln	Lys	Leu	Leu	Val	His	Cys	Gln	Lys	Leu
			165						170					175	
Lys	Asn	Thr	Glu	Met	Val	Ile	Ser	Val	Leu	Leu	Ser	Val	Ala	Glu	Leu
			180					185					190		
Tyr	Trp	Arg	Ser	Ser	Ser	Pro	Thr	Ile	Ala	Leu	Pro	Met	Leu	Leu	Gln
		195					200					205			
Ala	Leu	Ala	Leu	Ser	Lys	Glu	Tyr	Arg	Leu	Gln	Tyr	Leu	Ala	Ser	Glu
	210					215					220				
Thr	Val	Leu	Asn	Leu	Ala	Phe	Ala	Gln	Leu	Ile	Leu	Gly	Ile	Pro	Glu
225					230					235					240
Gln	Ala	Leu	Ser	Leu	Leu	His	Met	Ala	Ile	Glu	Pro	Ile	Leu	Ala	Asp
				245					250					255	
Gly	Ala	Ile	Leu	Asp	Lys	Gly	Arg	Ala	Met	Phe	Leu	Val	Ala	Lys	Cys
		260						265					270		
Gln	Val	Ala	Ser	Ala	Ala	Ser	Tyr	Asp	Gln	Pro	Lys	Lys	Ala	Glu	Ala
		275					280								
Leu	Glu	Ala	Ala	Ile	Glu	Asn	Leu	Asn	Glu	Ala	Lys	Asn	Tyr	Phe	Ala
	290					295					300				
Lys	Val	Asp	Cys	Lys	Glu	Arg	Ile	Arg	Asp	Val	Val	Tyr	Phe	Gln	Ala

*[The page contains extremely faint, illegible text.]*

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1540 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

- 51 -

AAACAACCTG TCCTGTTTTG TCAGTTCCCA GCTTCTTCGT TTAGAATAAA TTAGACCAAA	1020
AGAAGAAACG TGCTTGTCTC TGTATACCCG CAGAATGAAG TTACTGTTGT TAAAACCGGA	1080
TTTTTTCATT TTACTAGGTT CCGAAGAGTC CAGATGCTTG GTAGATGTTC AATACGTGAT	1140
TTTTTTTTTTA ATTGAATGTG TTCATTTAAA ATCCTCCTTA ACATTTCTAG AAAGACTTCT	1200
TTCAATAAAT AATGGAATCT TAGAGGAAAA GTGGTTTTTT AAAAGCTAGG GAACTCCTCC	1260
ACTAAAAGTA ACCATTGGAA ACCTCGAATG AGGGCTAAAG TTTTAATCAT AAGAGAAAAG	1320
GCAGCATAAT GAAATGTGTA CACATACATA GTCAGTGGTC CATTTTAGGA AGCCAGTGGC	1380
GTCTGATAAA GAAATGTTAA GAGTAGTGAG GTTGAGGAAG GAAATTGTGG GGATTTGAAA	1440
TATTCTCTTT ATGTTGTTTC TCTTCTGAGT CATGGTAAAA CAATAAATTA TCATCTCTAG	1500
GTGGCAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	1540

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 64 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Met	Lys	Leu	Leu	Leu	Leu	Lys	Pro	Asp	Phe	Phe	Ile	Leu	Leu	Gly	Ser
1					5				10					15	
Glu	Glu	Ser	Arg	Cys	Leu	Val	Asp	Val	Gln	Tyr	Val	Ile	Phe	Phe	Leu
			20					25						30	
Ile	Glu	Cys	Val	His	Leu	Lys	Ser	Ser	Leu	Thr	Phe	Leu	Glu	Arg	Leu
			35				40					45			
Leu	Ser	Ile	Asn	Asn	Gly	Ile	Leu	Glu	Glu	Lys	Trp	Phe	Phe	Lys	Ser
			50			55					60				

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

ANTGACGCCTT TAGCTAGTCC TTCTATCA

29

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

TNCAACAGTAT CAACCAGAAG TGCCAATC

29

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GNAAACAGTAT TAAATTGCAG AGTTCCAG

29

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

CNAATCATCAT CTCGCTTACA CAGTCAGG

29

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

ANCGAGACAGA CCAAGGCTCA CAGGTGAA

29

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GNGGACACACA CTCATAAAAC AGAAAATA

29

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

ANTAACCATAG AGTTTGGCTG GAGACCAC

29

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

ANTCTTCCGAT GGCAACACCA GCCTGCTT

29

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GNTCACCATTT CTGTGTTCTT CAGTTTCT

29

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

ANATTTAGGCT TATGCTGACC TCGTTGTA

29

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 162 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Met Gly Asn Ala Ser Tyr Ser Asp Ser Tyr Leu Glu Gly Ile Leu Leu  
1 5 10 15  
Lys Gly Val Phe Thr Cys Glu Pro Trp Ser Val Ser Val Gly Trp Ser  
20 25 30  
Thr Ser Val Asp Cys Gly Trp Phe Gln Ser Ala Trp Leu Arg Ser Ser  
35 40 45  
Thr Glu Gly Ser Thr Gly Ala Ala Leu Trp Gln Arg Leu Arg Arg Glu  
50 55 60  
Met Asp Gln Pro Thr Pro Gly Thr Trp Leu His Gly Ile Arg Lys Gly  
65 70 75 80  
Arg Cys Trp Pro Leu Cys Ser Cys Cys Leu Phe Leu Phe Leu Phe Ala  
85 90 95  
Phe Asp Leu Val Ala Thr Asp Arg Val Ala Arg Asp Leu Val Phe Ser  
100 105 110  
Ser Arg His Pro Ser Thr Pro Ala Leu Ser Gln Val Ser Cys Cys His  
115 120 125  
Ala Asn Ala Met Ser Thr Leu Ala Pro Arg Pro Lys Ser Val Gln Arg  
130 135 140  
Trp Pro Thr Xaa Ser Ser His Tyr Ser Leu Asn Ser Met Tyr His Leu  
145 150 155 160  
Pro Leu

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 83 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Leu Val Gly Gly Pro Phe Leu Pro Pro Thr Ser Val Cys Cys Ser Cys  
1 5 10 15  
Gln Lys Thr Cys Leu Leu Leu Pro Ala Glu Arg Glu Gln Ser Pro Glu  
20 25 30

His His Gln Glu Cys Leu Leu Val Tyr Trp Gln Leu Ala Thr Pro Ser  
 35 40 45  
 Ser Pro Phe Thr Gln Thr Arg Gly Arg Asp Gly Lys Gly Phe Phe Thr  
 50 55 60  
 Glu His Ser Gly Thr Pro Tyr Arg Arg Lys Leu Asp Arg Leu Val Asn  
 65 70 75 80  
 Gly Phe Ser

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1521 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

GTAACCTTCT TCTGCGCGGC TGCAGCTCGG GACTTCGGCC TGACCCAGCC CCCATGGCTT	60
CAGAAGAGCT ACAGAAAGAT CTAGAAGAGG TAAAGGTGTT GCTGGAAAAG GCTACTAGGA	120
AAAGAGTACG TGATGCCCTT ACAGCTGAAA AATCCAAGAT TGAGACAGAA ATCAAGAACA	180
AGATGCAACA GAAATCACAG AAGAAAGCAG AACTTCTTGA TAATGAAAAA CCAGCTGCTG	240
TGGTTGCTCC CATAACAACG GGCTATACGG TGAAAATCAG TAATTATGGA TGGGATCAGT	300
CAGATAAGTT TGTGAAAATC TACATTACCT TAACTGGAGT TCATCAAGTT CCCACTGAGA	360
ATGTGCAGGT GCATTTTACA GAGAGGTCAT TTGATCTTTT GGTAAAGAAT CTAAATGGGA	420
AGAGTTACTC CATGATTGTG AACAACTCTCT TGAAACCCAT CTCTGTGGAA GGCAGTTCAA	480
AAAAAGTCAA GACTGATACA GTTCTTATAT TGTGTAGAAA GAAAGTGGAA AACACAAGGT	540
GGGATTACCT GACCCAGGTT GAAAAGGAGT GCAAAGAAAA AGAGAAGCCC TCCTATGACA	600
CTGAAACAGA TCCTAGTGAG GGATTGATGA ATGTTCTAAA GAAAATTTAT GAAGATGGAG	660
ACGATGATAT GAAGCGAACC ATTAATAAAG CCTGGGTGGA ATCAAGAGAG AAGCAAGCCA	720
AAGGAGACAC GGAATTTTGA GACTTTAAAG TCGTTTTGGG AACTGTGATG TGATGTGGAA	780
ATACTGATGT TTCCAGTAAG GGAATATTGG TGAGCTGCAT ATATAAATTT GACAGATAGC	840
TATTTACATA GCCTTCTAAG TAAAGGCAAT GAATTCTCCA TTTCCTACTG GAGGATTTAT	900
TTAAATAAAA TATGCTTATT AAACACTCCT GCAAAGATGG TTTTATTAGT ACCCTGGTCA	960

TTTTGTTCAA GGAAGGGTTA TATTGCATTC TCACGTGAAA TATAAAAAGC AAGTCTTGCC 1020  
 CAATAAAAAC GCTACATTGT GTGTATTTTT TGTTCAGCTA AGAATTGGAA AAGTATTTGC 1080  
 TTGCCTTTTA AGTTACTGAC ATCAGCTTCC ACCAGTGTA AAATTGAGTA AAACCTGAAG 1140  
 TTTTGCATAA AATGCAAATC GGTGCCTGTG CTTGAAGGTT GCTGTAGAGC ATCTGACCCC 1200  
 TTATTACCAC CTTAAGCAAT GTATATGCCA TGCATTACCA TGCAC TAATT CAATCACAGG 1260  
 TGTCTTCTATC TAGATTTAAA TATATTTGTC AATGAATGTG GAATAGAAAA TCTAAACATG 1320  
 ACAATAATAG ACATATCTTT GTATGGTACC AGTTAGTTTT GCCGTGGATC AGATGGTTTA 1380  
 TAAAAGTAAT AACCATAAAG CAAAAAATAA TTTGAAAGCC CGTCTATTCC TATGCTCAAT 1440  
 AAAGTTAAGT TTTTTTTCAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1500  
 AAAAAAAAAA AAAAAAAAAA A 1521

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Met	Ala	Ser	Glu	Glu	Leu	Gln	Lys	Asp	Leu	Glu	Glu	Val	Lys	Val	Leu
1				5					10					15	
Leu	Glu	Lys	Ala	Thr	Arg	Lys	Arg	Val	Arg	Asp	Ala	Leu	Thr	Ala	Glu
			20					25					30		
Lys	Ser	Lys	Ile	Glu	Thr	Glu	Ile	Lys	Asn	Lys	Met	Gln	Gln	Lys	Ser
		35					40					45			
Gln	Lys	Lys	Ala	Glu	Leu	Leu	Asp	Asn	Glu	Lys	Pro	Ala	Ala	Val	Val
	50					55					60				
Ala	Pro	Ile	Thr	Thr	Gly	Tyr	Thr	Val	Lys	Ile	Ser	Asn	Tyr	Gly	Trp
65					70					75				80	
Asp	Gln	Ser	Asp	Lys	Phe	Val	Lys	Ile	Tyr	Ile	Thr	Leu	Thr	Gly	Val
			85					90						95	
His	Gln	Val	Pro	Thr	Glu	Asn	Val	Gln	Val	His	Phe	Thr	Glu	Arg	Ser
			100					105					110		

Phe Asp Leu Leu Val Lys Asn Leu Asn Gly Lys Ser Tyr Ser Met Ile  
           115                                  120                                  125  
  
 Val Asn Asn Leu Leu Lys Pro Ile Ser Val Glu Gly Ser Ser Lys Lys  
           130                                  135                                  140  
  
 Val Lys Thr Asp Thr Val Leu Ile Leu Cys Arg Lys Lys Val Glu Asn  
 145                                  150                                  155                                  160  
  
 Thr Arg Trp Asp Tyr Leu Thr Gln Val Glu Lys Glu Cys Lys Glu Lys  
                                   165                                  170                                  175  
  
 Glu Lys Pro Ser Tyr Asp Thr Glu Thr Asp Pro Ser Glu Gly Leu Met  
                                   180                                  185                                  190  
 Asn Val Leu Lys Lys Ile Tyr Glu Asp Gly Asp Asp Asp Met Lys Arg  
           195                                  200                                  205  
  
 Thr Ile Asn Lys Ala Trp Val Glu Ser Arg Glu Lys Gln Ala Lys Gly  
           210                                  215                                  220  
  
 Asp Thr Glu Phe  
 225

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1394 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

TGCGTCATGC AGTGCGCCGG AGGAACTGTG CTCTTTGAGG CCGACGCTAG GGGCCCGGAA	60
GGGAAACTGC GAGGCGAAGG TGACCGGGGA CCGAGCATTT CAGATCTGCT CGGTAGACCT	120
GGTGCACCAC CACCATGTTG GCTGCAAGGC TGGTGTGTCT CCGGACACTA CCTTCTAGGG	180
TTTTCCACCC AGCTTTCACC AAGGCCTCCC CTGTTGTGAA GAATTCCATC ACGAAGAATC	240
AATGGCTGTT AACACCTAGC AGGGAATATG CCACCAAAC AAGAATTGGG ATCCGGCGTG	300
GGAGAACTGG CCAAGAACTC AAAGAGGCAG CATTGGAACC ATCGATGGAA AAAATATTTA	360
AAATTGATCA GATGGGAAGA TGGTTTGTG CTGGAGGGGC TGCTGTTGGT CTTGGAGCAT	420
TGTGCTACTA TGGCTTGGGA CTGTCTAATG AGATTGGAGC TATTGAAAAG GCTGTAATTT	480
GGCCTCAGTA TGTCAAGGAT AGAATTCATT CCACCTATAT GTACTTAGCA GGGAGTATTG	540
GTTTAACAGC TTTGTCTGCC ATAGCAATCA GCAGAACGCC TGTTCATG AACTTCATGA	600

TGAGAGGCTC TTGGGTGACA ATTGGTGTGA CCTTTCAGC CATGGTTGGA GCTGGAATGC	660
TGGTACGATC AATACCATAT GACCAGAGCC CAGGCCCAAA GCATCTTGCT TGGTTGCTAC	720
ATTCTGGTGT GATGGGTGCA GTGGTGGCTC CTCTGACAAT ATTAGGGGGT CCTCTTCTCA	780
TCAGAGCTGC ATGGTACACA GCTGGCATTG TGGGAGGCCT CTCCACTGTG GCCATGTGTG	840
CGCCCAGTGA AAAGTTTCTG AACATGGGTG CACCCCTGGG AGTGGGCCTG GGTCTCGTCT	900
TTGTGTCCTC ATTGGGATCT ATGTTTCTTC CACCTACCAC CGTGGCTGGT GCCACTCTTT	960
ACTCAGTGGC AATGTACGGT GGATTAGTTC TTTTCAGCAT GTTCCTTCTG TATGATACCC	1020
AGAAAGTAAT CAAGCGTGCA GAAGTATCAC CAATGTATGG AGTTCAAAAA TATGATCCCA	1080
TTAACTCGAT GCTGAGTATC TACATGGATA CATTAAATAT ATTTATGCGA GTTGCAACTA	1140
TGCTGGCAAC TGGAGGCAAC AGAAAGAAAT GAAGTGA CTC AGCTTCTGGC TTCTCTGCTA	1200
CATCAAATAT CTTGTTTAAT GGGGCAGATA TGCATTAAAT AGTTTGTACA AGCAGCTTTC	1260
GTTGAAGTTT AGAAGATAAG AAACATGTCA TCATATTTAA ATGTTCCGGT AATGTGATGC	1320
CTCAGGTCTG CCTTTTTTTC TGGAGAATAA ATGCAGTAAT CCTCTCCCAA ATAAGCACAA	1380
AAAAAAAAAA AAAA	1394

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Met	Leu	Ala	Ala	Arg	Leu	Val	Cys	Leu	Arg	Thr	Leu	Pro	Ser	Arg	Val
1				5					10					15	
Phe	His	Pro	Ala	Phe	Thr	Lys	Ala	Ser	Pro	Val	Val	Lys	Asn	Ser	Ile
			20					25					30		
Thr	Lys	Asn	Gln	Trp	Leu	Leu	Thr	Pro	Ser	Arg	Glu	Tyr	Ala	Thr	Lys
		35					40					45			
Thr	Arg	Ile	Gly	Ile	Arg	Arg	Gly	Arg	Thr	Gly	Gln	Glu	Leu	Lys	Glu
	50					55					60				
Ala	Ala	Leu	Glu	Pro	Ser	Met	Glu	Lys	Ile	Phe	Lys	Ile	Asp	Gln	Met



65	70	75	80
Gly Arg Trp Phe Val Ala Gly Gly Ala Ala Val Gly Leu Gly Ala Leu	85	90	95
Cys Tyr Tyr Gly Leu Gly Leu Ser Asn Glu Ile Gly Ala Ile Glu Lys	100	105	110
Ala Val Ile Trp Pro Gln Tyr Val Lys Asp Arg Ile His Ser Thr Tyr	115	120	125
Met Tyr Leu Ala Gly Ser Ile Gly Leu Thr Ala Leu Ser Ala Ile Ala	130	135	140
Ile Ser Arg Thr Pro Val Leu Met Asn Phe Met Met Arg Gly Ser Trp	145	150	155
Val Thr Ile Gly Val Thr Phe Ala Ala Met Val Gly Ala Gly Met Leu	165	170	175
Val Arg Ser Ile Pro Tyr Asp Gln Ser Pro Gly Pro Lys His Leu Ala	180	185	190
Trp Leu Leu His Ser Gly Val Met Gly Ala Val Val Ala Pro Leu Thr	195	200	205
Ile Leu Gly Gly Pro Leu Leu Ile Arg Ala Ala Trp Tyr Thr Ala Gly	210	215	220
Ile Val Gly Gly Leu Ser Thr Val Ala Met Cys Ala Pro Ser Glu Lys	225	230	235
Phe Leu Asn Met Gly Ala Pro Leu Gly Val Gly Leu Gly Leu Val Phe	245	250	255
Val Ser Ser Leu Gly Ser Met Phe Leu Pro Pro Thr Thr Val Ala Gly	260	265	270
Ala Thr Leu Tyr Ser Val Ala Met Tyr Gly Gly Leu Val Leu Phe Ser	275	280	285
Met Phe Leu Leu Tyr Asp Thr Gln Lys Val Ile Lys Arg Ala Glu Val	290	295	300
Ser Pro Met Tyr Gly Val Gln Lys Tyr Asp Pro Ile Asn Ser Met Leu	305	310	315
Ser Ile Tyr Met Asp Thr Leu Asn Ile Phe Met Arg Val Ala Thr Met	325	330	335
Leu Ala Thr Gly Gly Asn Arg Lys Lys	340	345	

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1908 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

GCTTTTTTTT	TTTTTTTTTG	TTGAGATGGG	GTCTCGCCAT	GTTTCCCACA	CTGATCTTGA	60
ACTCCTGGGC	TCCAGGAATT	CTCCTACTTT	GGCCTCCCAA	AGTGTTGGGA	ATATTGGCAT	120
GAACCACAGC	ACCTGACTTG	CATATTTGTG	AATTCCCCAA	ATTGCTTTTT	TTAAATTGAT	180
TTCTAATTTT	ATTCATTGT	TATGGGGAAC	ATACTTTGTA	TGGTTTCAAT	GTTTTAAAAAT	240
TAATTGAGAC	TTGTTTTATG	ACTTAGCATA	TGGTCTGTGT	TGAAGAAGGC	TCCATGTACA	300
CTTGAGAATA	ATATGTATAC	TGTGGTTGTT	GGGTGGATTT	TCTATGTATG	TTTARGTGAT	360
ATGGTTTTAT	AGTGTTGTTT	AARTCTTCTA	TTTTCTTCTT	TTTCTGCCCA	GTTTTATTTT	420
TGAAAGCATA	CTGARGTCTC	CAACTCARTG	CCTTAGCCTC	CTGAGCAGTT	GGGACTACAG	480
GCATACGCCA	CTACACCCAG	CAATTTTTTT	GTATTTTTCT	GTAGAGACAG	AGTTTCACCA	540
TGTTGCCTAG	GCTGGTCTCA	GATTCCTGGA	CTCAAGTGAT	CTCGATTCCC	GGCCTCTGCC	600
TCCCGGGGTG	CTGGGATTGC	AGGCATGAGC	TACTATGCCT	GGCAAATTTT	ATTTTTTCCTT	660
TTATTTTGTC	ACATAATTAA	AGCTACTCCA	GAATTCCCTT	GATTTCTGCT	TGCCTGGTAT	720
ATCTTTTTTC	CATTTTTTAA	CTGTCAGCCT	TTTTTGTGCC	TGTTAATCTA	AAGTATGTGT	780
TTCGTAGATA	ATATGTAGCT	GGATCATATT	TTAAAAATAT	TTATTCTGCC	AAGCTCTGTC	840
TTTTGATTGG	AGTATTCTTT	CATTTATGTT	TGTAATTACT	GATGAGGGGG	GCACTAATGT	900
CTGCTGTTTT	GCTATTTGTT	TCCCCATGTC	TTATGTCTTC	ATTACTGACT	TTTTTATTAA	960
ACAACTATTT	TCTTGGGTAC	CATTTTAAGT	CCCTCTCCCA	CTCATTTTTT	AATGTTTTTT	1020
TGTGTTTACT	TTGTTTTTTA	TTGTTTGCCC	TGATATTAAA	ATTAACATTT	TACCTTGAAA	1080
TAGTTGGCTT	CAGATTAATA	TCAACTTAGT	TTCAATAGCA	TAGGAAATTT	GCTTCACTAT	1140
ATTTCCATTT	TCTCCCCGTC	CTTTGTGCTA	TTATTACTAT	ACCAATTAGA	TCTCTACACA	1200
ATATAGGCAT	ATCAACACAT	TTTGTAATTA	TTTCCTTATC	CAGTTGTCTT	TTAATATAGA	1260
TCTGTGAAGA	AAAGTATTAC	ACAAATAGAT	CTATTCTGTT	TTTTATAATT	ATTTAATTAC	1320
CTTTGGTGGT	GCTGTTTATT	TTTCATGCAT	TTGAGTTACT	GTCTAGTATT	CATTCATTTT	1380
TCTCTGAATC	ACTCCCTTTA	GTATTGCTTG	TAGGGCAGGT	CTGCTAGCAT	TGAATTCCTT	1440

TAATTTTGT GACTCTGCAA ATGCCATAAT TTCTCTTTTG TTTGTGAAGG ATAGTTTTC	1500
TAGATACAGA ATTTGCAGTT GGCATTCTTT TTAGTTTAGC AGTTTGAAAA TATTTCCCAT	1560
TGTTGGCCGG GCACAGTGGC TCACGCCTGT GGTCCTAGCA CTTTGGGAGG CCGAGGCGGG	1620
CGGATCGTCT GGGGTCGGGA GTTCGGGACC GGCCTGGCCA ATATGGTGAG GCCCTGTTTC	1680
TGCTAAAATA TAAAAATTGG CTGGGCATGA TGGCGGGTGC CTCTAGTCCC AGCTGCTCGG	1740
GAGGCTGAGG TGGGGGAGTC GCTTGAGCCC GGGAGATGAT GGCTGTGGTG AGCCGGGATG	1800
GCGCCGCTGC ACTCCGGCCT GGGCGGCTGA GTGAGACTCC ATCCCCGAAA AAAAAAAAAA	1860
AAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAA	1908

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Met	Arg	Gly	Ala	Leu	Met	Ser	Ala	Val	Leu	Leu	Phe	Val	Ser	Pro	Cys
1				5					10					15	
Leu	Met	Ser	Ser	Leu	Leu	Thr	Phe	Leu	Leu	Asn	Asn	Tyr	Phe	Leu	Gly
			20					25					30		
Tyr	His	Phe	Lys	Ser	Leu	Ser	His	Ser	Phe	Phe	Asn	Val	Phe	Leu	Cys
		35					40					45			
Leu	Leu	Leu	Phe	Leu	Leu	Phe	Ala	Leu	Ile	Leu	Lys	Leu	Thr	Phe	Tyr
	50					55					60				
Leu	Glu	Ile	Val	Gly	Phe	Arg	Leu	Ile	Ser	Thr					
65					70					75					

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3076 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

CTTTTTTTTT	TTTTTCAAT	TTCATTTAGT	TCTGCCCTGA	TCTTG GTTAT	TTCCTTTTTT	60
TCTGCTGGGT	TTGGGTTTGG	TTTGTCTTA	TTTCTCTAGT	TCCTTGAGGT	GTGACCTTAR	120
AATGTCAATT	TGTGCTCTTT	CAATCTTTTT	GATGTAGGCG	TTGAGGGCTG	TGGACTTTTC	180
TCTTG GCACT	CCCTTTGGTG	TATCCCARAG	GTTTTGATAG	GTTGTGTCAT	TATTGCAATT	240
CAGTTTGAAG	AATTTCTTAA	TCTCCACCTT	GATTTTGT TT	TTGACCCAAT	GCTCATTCAG	300
GAGCAGGTTA	TTTACTTTCC	ATGTACTTGC	ATGGCTTTGA	AGCTTCCTTT	TGGAGTTGAT	360
TTCCAGTTTT	ATTCCACTGT	GATTTGAGAG	AGTGCTTTAC	ATAATTTCAA	TTTTCTTAAT	420
TTTATTAAGG	CTCGTTTTAT	GGCCTATAAT	ATGGTCTATC	TTGGAGAAAG	TTCCATGCAC	480
TGTAGAATAG	AATGTGTATT	CTGTGGTTGT	TGGATGAAAT	GTTCTGCATA	TATTCCTAGA	540
TTGCCTCCCC	ACAAAAGGTT	GCATCAATGT	CTGTGTTTCT	CTACACCATC	TCACCCTTGC	600
CAACTTCGGG	TTTCATCAGA	CCTTACTGAT	TGTCAGTATG	ATCTGTGAAA	CAAATCTCTC	660
AGTTTTGATT	TGCATTTTTT	AAATTATGAG	AGCTTGAACA	CCATTTTACA	TGTTTATTGG	720
CTGTTGTTAT	TTCCTTTTTG	AGATCTGTTC	GTTATATGCT	TTGCCCGTTT	TTCTGTTGGG	780
TGGTTATTAT	TTTTCTTATT	GAATGGTATA	AGCTCTTTGT	AAGTTAAGGA	CATTAGCCCT	840
TAGTCAGATA	TTTTGACTTA	GGTTTTAATT	TTTTTCCACA	CAGAAGTTTT	AAGCTCTGTG	900
GCAAATTTAT	CAGTCTTATA	TCACTACAGG	GTTATAAATA	TTAGYTATCA	CTTCGGGTTT	960
GTGTCTTGCT	TAGAAAGCMT	CATTTGAAGA	TTGTAAATGT	TAGTAAGTTT	CCCCATATTT	1020
TCCTCTAGGA	CTTCCATGGT	TTAATTTGTT	TTGTTTAAAY	TAGGAATTGG	CATTACATC	1080
CTYTTTTGTC	CCAGGTCTCA	GAGGTCCCTT	GTATCTTATA	GAGCAGTATT	GTTTTATGTT	1140
ATTTTCCCAT	GTATAATTTA	AAAACAAAAT	ACGTTGTTCA	AAACAAAATA	CAGTGGCAGC	1200
AGATAATGGC	AGTATCTCTG	TAACTGCTGG	TAAACTGTAT	TTCATAGTGA	AGTGTTTATA	1260
AACTAAAGAG	TCATTGATTT	GGTTTCCTGG	CTAATTAAAA	TCTGAATTCC	ATTTGAAGTT	1320
CCATTGAAAT	CATGGTTTTA	CTCTATAGCA	GTGGATGTTT	TTTCCCAACC	TTTCTGATAT	1380
TTTTTTCCTT	CCTGAGACAG	GGTCTTGCTC	TGTCACCTGG	GATGGAGTGT	AGTTGCACCA	1440
TCAAGGCTTA	CTGCAGTCTC	AACTCTCTGA	GCTCAAGTGA	TCCTGCCACC	TCAGCCTCTT	1500
GAGTAGCAAG	GATTACAGGC	ACCTACCACT	ATGCCTGGCT	AATTTTATA	TTTTTTGTAG	1560
AGATGGATTC	TCACTATGTT	GCCCGGGCTC	ATCTTGA ACT	CGAGCTCAAG	CAATCTGTCC	1620

ATCTTGGCCT	CCCAAAGTGC	TGGGATTATA	GGCGTGAGCC	ACTGCACCTG	GCCCCTTTCT	1680
GATTATTTTA	ATCTATCTTT	AAATGTTCAA	AGTGATTTCG	CTAATTCATT	TAAAGCATAT	1740
TTAGTTTTTT	TTAAATTGAG	TGTATTTTAT	CTAGATATTT	TTAAAAGGCA	GCATCTAACC	1800
TTGGATTTTA	TAAATACATC	TAAATTTGTT	ATTTCCAGAA	TGCTTCAAAA	CAGATCTCTG	1860
TAGCCTCGTG	CTTTGTTATT	GTTAGGTTTT	TTTTTTTTGT	TTTGAGACAG	GGTCTTGCTC	1920
TATCTGGAGT	GCAGTGGCAC	AGTCATAGCT	CACTGTACCC	TCAAACCTCCT	AAACTCAAGT	1980
AATCCTCCCA	TCTCAGCCTC	CTGAGTAGTT	GGGACCACAG	TCATGCACCA	GCATGCCTGG	2040
CTAATTTTTT	AAATTTTGTT	CTTAATAGAG	ACAGAGTCTT	GCTGTGTTGT	TCAGGCTGGT	2100
CTCAAACCTC	TGGGCTCAAG	CGATCCTCCC	ACCTCAGCCT	CCTAAAGTGC	TGAGATTACG	2160
GATGTGAATC	ATTACACCCA	GCCTATTAAT	GGTTTGTAT	AGCAAGTCTT	TTGTGGGTGG	2220
TGGAAAGATG	AAGTGCTGTG	AAATATTGTA	GGAGCAGAAA	CTTGAAATGT	GGCAAAAACC	2280
ACATGGGCAA	AATTTCTGTC	TCTTTTCTTA	TTTTTGCTTT	TTTGTTTAAA	GGTTTTTCTA	2340
TTGGGAAAGC	TACTGATCGG	ATGGATGCTT	TCAGGAAAGC	AAAGAACAGA	GCAGTTCACC	2400
ATTTGCATTA	TATAGAACGA	TATGAAGACC	ATACAATATT	CCATGATATT	TCATTAAGAT	2460
TTAAAAGGAC	GCATATCAAG	ATGAAGAAAC	AACCCAAAGG	TTACGGCCTC	CGCTGCCACA	2520
GGGCCATCAT	CACCATCTGC	CGGCTCATTG	GCATCAAAGA	CATGTATGCC	AAGGTCTCTG	2580
GGTCCATTAA	TATGCTCAGC	CTCACCAGG	GCCTCTTCCG	TGGGCTCTCC	AGACAGGAAA	2640
CCCATCAACA	GCTGGCTGAT	AAGAAGGGCC	TCCATGTTGT	GGAAATCCGG	GAGGAATGTG	2700
GCCCTCTGCC	CATTGTGGTT	GCGTCCCCCC	GGGGGCCCTT	GAGGAAGGAT	CCAGAGCCAG	2760
AAGATGAGGT	TCCAGACGTC	AAACTGGACT	GGGAAGATGT	GAAGACTGCA	CAGGGAATGA	2820
AGCGCTCTGT	GTGGTCTAAT	TTGAAGAGAG	CCGCCACGTA	ACCTCTCTGG	CCTTGTGCAG	2880
CCAGTTCCTG	TGCTGCCCTG	CACCTAGGAG	AGACTCAGCC	CCTCACAGCT	TGGGATGTTA	2940
CCTTGCCTTT	TGTTTGTTTT	GAGGGAAGTT	TAATCTTTAA	ACTCTTTGGA	AATAAATAAT	3000
TATAGCTTTC	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	3060
AAAAAAAAAA	AAAAAA					3076

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Met	Gly	Lys	Ile	Ser	Val	Ser	Phe	Leu	Ile	Phe	Ala	Phe	Leu	Phe	Lys	
1				5					10					15		
Gly	Phe	Ser	Ile	Gly	Lys	Ala	Thr	Asp	Arg	Met	Asp	Ala	Phe	Arg	Lys	
			20					25					30			
Ala	Lys	Asn	Arg	Ala	Val	His	His	Leu	His	Tyr	Ile	Glu	Arg	Tyr	Glu	
		35					40					45				
Asp	His	Thr	Ile	Phe	His	Asp	Ile	Ser	Leu	Arg	Phe	Lys	Arg	Thr	His	
	50					55					60					
Ile	Lys	Met	Lys	Lys	Gln	Pro	Lys	Gly	Tyr	Gly	Leu	Arg	Cys	His	Arg	
65					70					75					80	
Ala	Ile	Ile	Thr	Ile	Cys	Arg	Leu	Ile	Gly	Ile	Lys	Asp	Met	Tyr	Ala	
				85					90					95		
Lys	Val	Ser	Gly	Ser	Ile	Asn	Met	Leu	Ser	Leu	Thr	Gln	Gly	Leu	Phe	
			100					105					110			
Arg	Gly	Leu	Ser	Arg	Gln	Glu	Thr	His	Gln	Gln	Leu	Ala	Asp	Lys	Lys	
		115					120					125				
Gly	Leu	His	Val	Val	Glu	Ile	Arg	Glu	Glu	Cys	Gly	Pro	Leu	Pro	Ile	
		130				135					140					
Val	Val	Ala	Ser	Pro	Arg	Gly	Pro	Leu	Arg	Lys	Asp	Pro	Glu	Pro	Glu	
145					150					155					160	
Asp	Glu	Val	Pro	Asp	Val	Lys	Leu	Asp	Trp	Glu	Asp	Val	Lys	Thr	Ala	
			165						170				175			
Gln	Gly	Met	Lys	Arg	Ser	Val	Trp	Ser	Asn	Leu	Lys	Arg	Ala	Ala	Thr	
			180					185					190			

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 683 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

CGCCAAGTGC GCATGGGGAC GCTATAGCAA TTCGTTTGCT GTCCTTCCTC TCCTTCGAAG 60  
ATGACAAGGC CTACCATCGT TTCTTCCTGC CTTTGGGCCG TCAGGCAGTT GGTGTTGGGACC 120  
CGCTCCAACC CTCGGTTCTT CCTGCAATAC AGTGGATACA ATTTGTCATG GCTACTCTGA 180  
GTGTTATAGG TTCAAGTTCA CTTATTGCCT ATGCTGTATT CCATAATATA CAGAAATCTC 240  
CAGAGATAAG ACCACTTTTT TATCTGAGCT TCTGTGACCT GTCCTGGGA CTTTGCTGGC 300  
TCACGGAGAC ACTTCTCTAT GGAGCTTCAG TAGCAAATAA GGACATCATC TGCTATAACC 360  
TACAAGCAGT TGGACAGATA TTCTACATTT CCTCATTTCT CTACACCGTC AATTACATCT 420  
GGTATTTGTA CACAGAGCTG AGGATGAAAC ACACCCAGAG TGGACAGAGC ACATCTCCAC 480  
TGGTGATAGA TTATACTTGT CGAGTTGGTC AAATGGCCTT TGTTTTCTCA AGCCTGATAC 540  
CTCTGCTATT GATGACACCT GTATTCTGTC TGGGAAATAC TAGTGAATGT TTCCAAAAC 600  
TCAGTCAGAG CCACAAGTGT ATCTTGATGC ACTCACCACC ATCAGCCATG GCTGAACTTC 660  
CACCTTCTGC CAACACATCT GTC 683

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Met Ala Thr Leu Ser Val Ile Gly Ser Ser Ser Leu Ile Ala Tyr Ala  
1 5 10 15  
Val Phe His Asn Ile Gln Lys Ser Pro Glu Ile Arg Pro Leu Phe Tyr  
20 25 30  
Leu Ser Phe Cys Asp Leu Leu Leu Gly Leu Cys Trp Leu Thr Glu Thr  
35 40 45  
Leu Leu Tyr Gly Ala Ser Val Ala Asn Lys Asp Ile Ile Cys Tyr Asn  
50 55 60  
Leu Gln Ala Val Gly Gln Ile Phe Tyr Ile Ser Ser Phe Leu Tyr Thr  
65 70 75 80  
Val Asn Tyr Ile Trp Tyr Leu Tyr Thr Glu Leu Arg Met Lys His Thr

85

90

95

Gln	Ser	Gly	Gln	Ser	Thr	Ser	Pro	Leu	Val	Ile	Asp	Tyr	Thr	Cys	Arg
			100					105						110	
Val	Gly	Gln	Met	Ala	Phe	Val	Phe	Ser	Ser	Leu	Ile	Pro	Leu	Leu	Leu
		115					120					125			
Met	Thr	Pro	Val	Phe	Cys	Leu	Gly	Asn	Thr	Ser	Glu	Cys	Phe	Gln	Asn
		130					135					140			
Phe	Ser	Gln	Ser	His	Lys	Cys	Ile	Leu	Met	His	Ser	Pro	Pro	Ser	Ala
145					150					155					160
Met	Ala	Glu	Leu	Pro	Pro	Ser	Ala	Asn	Thr	Ser	Val				
				165					170						

## (2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 524 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

ATATGGCTGG	ACGCAGCACA	AATTCCACCA	ACTAAAGCAG	GAGGCTCGGC	GTGATGCAGA	60
TACCCAGACA	CCATTATTAT	GCTCACAGAA	GAGATTCTAT	AGCAGGGGCT	TAAATTCACT	120
GGAATCCACC	CTGACTTTTC	CTGCCAGTAC	TTCTACCATT	TTTTGAAACT	ACAATACTGG	180
AACATCCAGG	AACTGGAGTT	ATTCTACGCT	AATGGATTGG	AAAGAATGTT	GGGAAAGGAC	240
ATCTTAAATC	TTTTCTAACT	ATGCCCTAAA	CTGCAGAACT	CAAAGGAAAT	ATAGTGCCAT	300
TGTTAGTAGT	CATTCTAGAT	GAATTGGGAG	TATCTCTCCA	GTTATTCCCA	GATTCACTAG	360
TGATCCTTAA	AGTCTCTATT	CAGGGAGAGG	AAGACACTTT	CCATCTCAGA	GATAGACTCG	420
TGTTACCTTG	ATGGATATTG	GATTTGTCTA	AGTCTCTTCT	AGAAAAAATA	AATTCTAGAT	480
TATTAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAA		524

## (2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2171 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear



(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

CCCCGCTACC GGGTTGCGGC CGGAAGCCGG GCGCCGCGGC TCTGCTTCCC TCGGGGATCT	60
GGCGACATGG CCAGAAAGGC TCTCAAGCTT GCTTCGTGGA CCAGCATGGC TCTTGCTGCC	120
TCTGGCATCT ACTTCTACAG TAACAAGTAC TTGGACCCTA ATGACTTTGG CGCTGTCAGG	180
GTGGGCAGAG CAGTTGCTAC GACGGCTGTC ATCAGTTACG ACTACCTCAC TTCCCTGAAG	240
AGTGTCCCTT ATGGCTCAGA GGAGTACTTG CAGCTGAGAT CTAAGGTGCA CCTTCGCTCT	300
GCCAGGCGTC TCTGTGAGCT CTGCTGTGCC AACCGGGGCA CCTTCATCAA GGTGGGCCAG	360
CACCTGGGGG CTCTGGACTA CCTGTTGCCA GAGGAGTACA CCAGCACGCT GAAGGTACTG	420
CACAGCCAGG CTCCACAGAG CAGCATGCAA GAGATCCGCC AGGTCATCCG AGAAGATCTG	480
GGCAAGGAGG TGCTCGTTCT GGCTGTGAAG CAGCTGTTCC CAGAGTTTGA GTTTATGTGG	540
CTTGTGGATG AAGCCAAGAA GAACCTGCCT TTGGAGCTGG ATTCCTCAA TGAAGGGAGG	600
AATGCTGAGA AGGTGTCCCA GATGCTCAGG CATTTTGA CTCTGAAGGT CCCCCGAATC	660
CACTGGGACC TGTCCACGGA GCGGGTCCTC CTGATGGAGT TTGTGGATGG CGGGCAGGTC	720
AATGACAGAG ACTACATGGA GAGGAACAAG ATCGACGTCA ATGAGGTGAG GTCAAGAGCT	780
CAGGGCTGCT GTGCCGGGGA ACGTGGGCTT GGTCAAGGCT GCCCAGGAAG TGCCTGTGTG	840
TCCAGATCTC ACGCCACCTG GGCAAGATGT ATAGTGAGAT GATCTTCGTC AATGGCTTCG	900
TGCACTGCGA TCCCCACCCC GGCAATGTAC TGGTGCGGAA GCACCCCGGC ACGGGAAAGG	960
CGGAGATTGT CCTGTTGGAC CATGGGCTTT ACCAGATGCT CACGGAAGAA TTCCGCCTGA	1020
ATTACTGCCA CCTCTGGCAG TCTCTGATCT GGACTGACAG GAAGAGAGTG AAGGAGTACA	1080
GCCAGCGACT GGGAGCCGGG GATCTCTACC CCTTGTTTGC CTGCATGCTG ACGGCGCGAT	1140
CGTGGGACTC GGTCAACAGA GGCATCAGCC AAGCTCCCGT CACTGCCACT GAGGACTTAG	1200
AGATTCGCAA CAACGCGGCC AACTACCTCC CCCAGATCAG CCATCTCCTC AACCACGTGC	1260
CGCGCCAGAT GCTGCTCATC TTGAAGACCA ACGACCTGCT GCGTGGCATT GAGGCCGCCC	1320
TGGGCACCCG CGCCAGCGCC AGCTCCTTTC TCAACATGTC ACGTTGCTGC ATCAGAGCGC	1380
TAGCTGAGCA CAAGAAGAAG AATACCTGTT CATCTTCAG AAGGACCCAG ATCTCTTTCA	1440
GCGAGGCCTT CAACTTATGG CAGATCAACC TCCATGAGCT CATCCTGCGT GTGAAGGGGT	1500
TGAAGCTGGC TGACCGGGTC TTGGCCCTAA TATGCTGGCT GTTCCCTGCT CCACTCTGAG	1560

TGGAATTGCT CTCCCTGCCC CATTCTGGTG TCTTTCCACT CCTCAGCCCC TCATCTTGCC 1620  
 TCCACCCAGC TGCTCCATTT TTGCCACATC GTGGCCCGCA GCCCCAGAGT CACTGTCCAT 1680  
 GTCACCATCC TCCTCCTCCT TTGGAATCCT CTCCGCACAC TGTGGCCCTT GTCTCAGGGC 1740  
 CCACAAGCTG AACTGTGGCA TAGCTCTCTC TTCTTCTCCA AGAAGACTCA GCAGCCTACA 1800  
 TTCCCATTC TGGTATGTGC CATTGGGTTG GATGTCCCCA CTACTTCCGT TAACCCTTCC 1860  
 CATTGTCAAG ATGTGCCACG GGTGCCACTG GGGGCACACT GAACTTGTAG GGAGTGTGAT 1920  
 TTTGTTGGAG GTGCACATGG TCTCTGAATT TGACAGAGAA CACCTTCCCT TTCCTTGCCA 1980  
 TGTCACCCTC CAGAGGAAGT CACACCTCAG CGAGGTGGTT TGGCATCTGG GGCCAACTCC 2040  
 ATTACAGCTA TGAGCTCACT GCTGTCACTG ACGTTTGGTG TTTTCTGTAC TGTGTTTCAA 2100  
 TAAAACTCC TTCAAGGTTG CAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 2160  
 AAAAAAAAAA A 2171

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Met Ala Arg Lys Ala Leu Lys Leu Ala Ser Trp Thr Ser Met Ala Leu  
 1 5 10 15  
 Ala Ala Ser Gly Ile Tyr Phe Tyr Ser Asn Lys Tyr Leu Asp Pro Asn  
 20 25 30  
 Asp Phe Gly Ala Val Arg Val Gly Arg Ala Val Ala Thr Thr Ala Val  
 35 40 45  
 Ile Ser Tyr Asp Tyr Leu Thr Ser Leu Lys Ser Val Pro Tyr Gly Ser  
 50 55 60  
 Glu Glu Tyr Leu Gln Leu Arg Ser Lys Val His Leu Arg Ser Ala Arg  
 65 70 75 80  
 Arg Leu Cys Glu Leu Cys Cys Ala Asn Arg Gly Thr Phe Ile Lys Val  
 85 90 95  
 Gly Gln His Leu Gly Ala Leu Asp Tyr Leu Leu Pro Glu Glu Tyr Thr  
 100 105 110

Ser Thr Leu Lys Val Leu His Ser Gln Ala Pro Gln Ser Ser Met Gln	
115 120 125	
Glu Ile Arg Gln Val Ile Arg Glu Asp Leu Gly Lys Glu Val Leu Val	
130 135 140	
Leu Ala Val Lys Gln Leu Phe Pro Glu Phe Glu Phe Met Trp Leu Val	
145 150 155 160	
Asp Glu Ala Lys Lys Asn Leu Pro Leu Glu Leu Asp Phe Leu Asn Glu	
165 170 175	
Gly Arg Asn Ala Glu Lys Val Ser Gln Met Leu Arg His Phe Asp Phe	
180 185 190	
Leu Lys Val Pro Arg Ile His Trp Asp Leu Ser Thr Glu Arg Val Leu	
195 200 205	
Leu Met Glu Phe Val Asp Gly Gly Gln Val Asn Asp Arg Asp Tyr Met	
210 215 220	
Glu Arg Asn Lys Ile Asp Val Asn Glu Val Arg Ser Arg Ala Gln Gly	
225 230 235 240	
Cys Cys Ala Gly Glu Arg Gly Leu Gly Gln Gly Cys Pro Gly Ser Ala	
245 250 255	
Cys Val Ser Arg Ser His Ala Thr Trp Ala Arg Cys Ile Val Arg	
260 265 270	

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1613 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

CATGGCGGCT CCCTTGGTCC TGGTGCTGGT GGTGGCTGTG ACAGTGC GGG CGGCCTTGTT	60
CCGCTCCAGT CTGGCCGAGT TCATTTCCGA GCGGGTGGAG GTGGTGTCCC CACTGAGCTC	120
TTGGAAGAGA GTGGTTGAAG GCCTTTCACT GTTGGACTTG GGAGTATCTC CGTATTCTGG	180
AGCAGTATTT CATGAACTC CATTAATAAT ATACCTCTTT CATTTCTTAA TTGACTATGC	240
TGAATTGGTG TTTATGATAA CTGATGCACT CACTGCTATT GCCCTGTATT TTGCAATCCA	300
GGACTTCAAT AAAGTTGTGT TTAAAAAGCA GAACTCCTC CTAGAACTGG AACAGTATGC	360

CCCAGATGTG GCCGAACTCA TCCGGACCCC TATGGAAATG CGTTACATCC CTTTGAAAGT	420
GGCCCTGTTC TATCTCTTAA ATCCTTACAC GATTTTGTCT TGTGTTGCCA AGTCTACCTG	480
TGCCATCAAC AACACCCTCA TTGCTTTCTT CATTTTGA CTGATAAAAAG TTTCATTATC	540
TGTAAAATGG GGACAGTAAT TGTACCCACT TCATGGAATT ATTGAGAAGA CTAAATGGCT	600
TAAGGCAGTG CTTTCCTCAG TGCTATTTTT CTTGCCTTAG CGACATACCA GTCTCTGAAC	660
CCACTCACCT TGTTTGTCCC AGGACTCCTC TATCTCCTCC AGCGGCAGTA CATACTGTG	720
AAAATGAAGA GCAAAGCCTT CTGGATCTTT TCTTGGGAGT ATGCCATGAT GTATGTGGGA	780
AGCCTAGTGG TAATCATTTG CCTCTCCTTC TTCCTTCTCA GCTCTTGGGA TTTCATCCCC	840
GCAGTCTATG GCTTTATACT TTCTGTTCCA GATCTCACTC CAAACATTGG TCTTTTCTGG	900
TACTTCTTGG CAGAGATGTT TGAGCACTTC AGCCTCTTCT TTGTATGTGT GTTTCAGATC	960
AACGTCTTCT TCTACACCAT CCCCTTAGCC ATAAAGCTAA ATCCTGAGAA ACATCTTTGT	1020
CCTCACCTGC ATCATCATCG TCTGTTCCCT GCTCTTCCCT GTCCTGTGGC ACCTCTGGAT	1080
TTATGCAGGA AGTGCCAACT CTAATTTCTT TTATGCCATC AACTGACCT TCAACGTGG	1140
GCAGATCCTG CTCATCTCTG ATTACTTCTA TGCCTTCCTG CGGCGGGAGT ACTACCTCAC	1200
ACATGGCCTC TACTTGACCG CCAAGGATGG CACAGAGGCC ATGCTCGTGC TCAAGTAGGC	1260
CTGGCTGGCA CAGGGCTGCA TGGACCTCAG GGGGCTGTGG GGCCAGAAGY TGGGCCAAGC	1320
CCTCCAGCCA GAGTTGCCAG CAGGCGAGTG CTTGGGCAGA AGAGGTTCTGA GTCCAGGGTC	1380
ACAAGTCTCT GGTACCAAAA GGGACCCATG GCTGACTGAC AGCAAGGCCT ATGGGGAAGA	1440
ACTGGGAGYT CCCCAACTTG GACCCCCACC TTGTGGCTCT GCACACCAAG GAGCCCCYTC	1500
CCAGACAGGA AGGAGAAGAG GCAGGTGAGC AGGGCTTGTT AGATTGTGGC TACTTAATAA	1560
ATGTTTTTTT TTATGAAGTC TAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAA	1613

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 185 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Met Ala Ala Pro Leu Val Leu Val Leu Val Val Ala Val Thr Val Arg

1	5	10	15
Ala Ala Leu Phe Arg Ser Ser Leu Ala Glu Phe Ile Ser Glu Arg Val			
20	25	30	
Glu Val Val Ser Pro Leu Ser Ser Trp Lys Arg Val Val Glu Gly Leu			
35	40	45	
Ser Leu Leu Asp Leu Gly Val Ser Pro Tyr Ser Gly Ala Val Phe His			
50	55	60	
Glu Thr Pro Leu Ile Ile Tyr Leu Phe His Phe Leu Ile Asp Tyr Ala			
65	70	75	80
Glu Leu Val Phe Met Ile Thr Asp Ala Leu Thr Ala Ile Ala Leu Tyr			
85	90	95	
Phe Ala Ile Gln Asp Phe Asn Lys Val Val Phe Lys Lys Gln Lys Leu			
100	105	110	
Leu Leu Glu Leu Glu Gln Tyr Ala Pro Asp Val Ala Glu Leu Ile Arg			
115	120	125	
Thr Pro Met Glu Met Arg Tyr Ile Pro Leu Lys Val Ala Leu Phe Tyr			
130	135	140	
Leu Leu Asn Pro Tyr Thr Ile Leu Ser Cys Val Ala Lys Ser Thr Cys			
145	150	155	160
Ala Ile Asn Asn Thr Leu Ile Ala Phe Phe Ile Leu Thr Thr Ile Lys			
165	170	175	
Val Ser Leu Ser Val Lys Trp Gly Gln			
180	185		

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 372 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

AAACCCTGTC GGTCTTGGAG CGACGACGGC AGAACCAGGG TCCCTGGCGG TGCGGCGGGG	60
CCGGCGGGTG CAGCGGAAGC GGCGGCGGCG GCGGCAGTGA CGTCGCCGGG AACCTAAGG	120
ACTCTGCAAT ATGAATAATT CCCTAGAGAA CACCATCTCC TTTGAAGAGT ACATCCGAGT	180
AAAGGCACGG TCTGTCCCGC AACACAGGAT GAAGGAATTT CTGGACTCAC TGGCCTCTAA	240

GGGGCCAGAA GCCCTTCAGG AGTTCCAGCA GACAGCCACC ACTACCATGG TGTACCAACA	300
GGGTGGGAAC TGCATATACA CAGACAGCAC TGAAGTGGCT GGGTCTTTGC TTGAACTTGC	360
CTGTCCAATC AC	372

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 602 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

CGGGAAGCTC GAAATGGAGA AGGTGAACCT TATGACCCAG ATGTGCTCTA CTATATTTTC	60
CTGTGTATTC AAAAGTATCT TTTTGAAAT GGAAGGGTAG ATGACATTTT CTCCGATCTT	120
TATTATGTTC GGTTCACGGA GTGGCTACAT GAAGTTCTGA AGGATGTTCA GCCCCGGGTC	180
ACTCCACTTG GCTATGTCTT GCCCAGCCAC GTGACTGAGG AGATGCTATG GGAGTGCAAG	240
CAGCTTGGGG CTCACTCCCC CTCCACCTTG CTGACCACCC TCATGTTCTT TAATACCAAG	300
TAAGTGTTCT AGAGGCTCCA CTGCTGGCAT CTGTCCAGTG AAGAGTGTGG AAACCTATCCA	360
AGAGGCCTTC TGAATTCCTC TGACATATAT TTGAGAACT GGGCTACTGA AAGCCCTAAC	420
CCCACTTGGC TGCATTTTAT TTGGTAACCA GTGAGGCAAA CACCCTTGCC AGACCCCTAC	480
CATCCATCTT GATGTGGTTC CTGCACTGGA CACTGCTTGG GTACGGGCCT GCCCAGATCT	540
TGGGAATGTG GGCAGTGGCT CCTCTGAAGC ACCAGTGGGC AGAGGATGAG TCATGGTATC	600
CT	602

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Met Trp Phe Leu His Trp Thr Leu Leu Gly Tyr Gly Pro Ala Gln Ile  
 1 5 10 15  
 Leu Gly Met Trp Ala Val Ala Pro Leu Lys His Gln Trp Ala Glu Asp  
 20 25 30  
 Glu Ser Trp Tyr Pro  
 35

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 483 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

TGGGAAAGGG CTTGGACTGT GAAAAGAAAT GTGGCCCCCTT TCCATCTTCA AGAGAGATGG	60
AATTAATGAT GGATGGACCC TGGAGGGAAT CTCCCCAGCC GACTTCCACT GGGCTGACAG	120
ACTTTGCTGA CCACAGGGGA ACGATGTTCT TTTCTTTCTT CATGATCAGA CATAAACTTA	180
GCATTTTAAT GGAAGAAAAA TGAGGGGAAC TTCAATTATG ATTTATTAAA GACAATTTCT	240
ATTACACCTT CCTTTATGAC AAGTGACATT TTAGATGTAA AAGTAAAAAC TTTACCATGC	300
CTTTTTTTTT TTTGTTGGCC TAACATTGAG GCCTTAAAAC CTGAGGCTCC TGTGCCTGAT	360
GGAATTCTTG TAACATACAC TTGTGTATCA TATAAGATA CCACTCTGTT TCTCTTATGT	420
ATTCTTACTC TAGTTGTTTA TTAAGAATGA CAAGCACGTC TTTTCAACAA AAAAAAAAAA	480
AAA	483

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1853 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

CAGATTGCT	GCTGGAGTGC	TGGATGGAGC	CTTTCTCTGC	CCTCTGTGAC	ATTTCCAATT	60
TTAGATAATG	CCTCACATCT	CTGTCCCCC	GGGACCCCT	GGAGCCCCCA	TGATCCCTAA	120
GAAGACAGCT	TGAACCTAGA	TCTCACCCC	AGGATGTTGC	GGAGGCTGCT	GGAGCGGCCT	180
TGCACGCTGG	CCCTGCTTGT	GGGCTCCCAG	CTGGCTGTCA	TGATGTACCT	GTCACCTGGG	240
GGCTTCCGAA	GTCTCAGTGC	CCTATTTGGC	CGAGATCAGG	GACCGACATT	TGACTATTCT	300
CACCCTCGTG	ATGTCTACAG	TAACCTCAGT	CACCTGCCTG	GGGCCCCAGG	GGGTCCTCCA	360
GCTCCTCAAG	GTCTGCCCTA	CTGTCCAGAA	CGATCTCCTC	TCTTAGTGGG	TCCTGTGTCTG	420
GTGTCCTTTA	GCCCAGTGCC	ATCACTGGCA	GAGATTGTGG	AGCGGAATCC	CCGGGTAGAA	480
CCAGGGGGCC	GGTACCGCCC	TGCAGGTTGT	GAGCCCCGCT	CCCGAACAGC	CATCATTGTG	540
CCTCATCGTG	CCCGGGAGCA	CCACCTGCGC	CTGCTGCTCT	ACCACCTGCA	CCCCTTCTTG	600
CAGCGCCAGC	AGCTTGCTTA	TGGCATCTAT	GTCATCCACC	AGGCTGGAAA	TGGAACATTT	660
AACAGGGCAA	AACTGTTGAA	CGTTGGGGTG	CGAGAGGCC	TGCGTGATGA	AGAGTGGGAC	720
TGCCTGTTCT	TGCACGATGT	GGACCTCTTG	CCAGAAAATG	ACCACAATCT	GTATGTGTGT	780
GACCCCGGG	GACCCCGCCA	TGTTGCCGTT	GCTATGAACA	AGTTTGGATA	CAGCCTCCCCG	840
TACCCCAAGT	ACTTCGGAAG	AGTCTCAGCA	CTTACTCCTG	ACCAGTACCT	GAAGATGAAT	900
GGCTTCCCCA	ATGAATACTG	GGGCTGGGGT	GGTGAGGATG	ACGACTTGCT	ACCAGGGTGC	960
GCCTGGCTGG	GATGAAGATC	TCTCGGCCCC	CCACATCTGT	AGGACACTAT	AAGATGGTGA	1020
AGCACCGAGG	AGATAAGGGC	AATGAGGAAA	ATCCCCACAG	ATTTGACCTC	CTGGTCCGTA	1080
CCCAGAATTC	CTGGACGCAA	GATGGGATGA	ACTCACTGAC	ATACCAGTTG	CTGGCTCGAG	1140
AGCTGGGGCC	TCTTTATACC	AACATCACAG	CAGACATTGG	GACTGACCCT	CGGGGTCCTC	1200
GGGCTCCTTC	TGGGCCACGT	TACCCACCTG	GTTCCCTCCA	AGCCTTCCGT	CAAGAGATGC	1260
TGCAACGCCG	GCCCCAGCC	AGGCCTGGGC	CTCTATCTAC	TGCCAACCAC	ACAGCCCTCC	1320
GAGGTTCACA	CTGACTCCTC	CTTCCTGTCT	ACCTTAATCA	TGAAACCGAA	TTCATGGGGT	1380
TGTATTCTCC	CCACCCTCAG	CTCCTCACTG	TTCTCAGAAG	GATGTGAGGG	AACTGAACTC	1440
TGGTGCCGTG	CTAGGGGGTA	GGGGCCTCTC	CCTCACTGCT	GGACTGGAGC	TGGGCTCCTG	1500
TAGACCTGAG	GGTCCNTCTY	TCTAGGTCTC	CTGTAGGGCT	TAKGACTGTG	AATCCTTGAT	1560
GTCATGATTT	TATGTGACGA	TTCCTAGGAG	TCCCTGCCCC	TAGAGTAGGA	GCAGGGYTGG	1620
ACCCAAGCC	CNTCCYTYTT	CCATGGAGAG	AAGAGTGATC	TGGYTTCTCC	TCGGACCTCT	1680
GTGAATATTT	ATTCTATTTA	TGGTTCCCGG	GAAGTTGTTT	GGTGAAGGAA	GCCCCCCCC	1740



TGGGCATTTT CTGCCTATGC TGGAATAGCT CCCTCTTCTG GTCCTGGCTC AGGGGGCTGG 1800  
 GATTTTGATA TATTTTCTAA TAAAGGACTT TGTCTCGCAA AAAAAAAAAA AAA 1853

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 273 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Met	Leu	Arg	Arg	Leu	Leu	Glu	Arg	Pro	Cys	Thr	Leu	Ala	Leu	Leu	Val	1	5	10	15
Gly	Ser	Gln	Leu	Ala	Val	Met	Met	Tyr	Leu	Ser	Leu	Gly	Gly	Phe	Arg	20	25	30	
Ser	Leu	Ser	Ala	Leu	Phe	Gly	Arg	Asp	Gln	Gly	Pro	Thr	Phe	Asp	Tyr	35	40	45	
Ser	His	Pro	Arg	Asp	Val	Tyr	Ser	Asn	Leu	Ser	His	Leu	Pro	Gly	Ala	50	55	60	
Pro	Gly	Gly	Pro	Pro	Ala	Pro	Gln	Gly	Leu	Pro	Tyr	Cys	Pro	Glu	Arg	65	70	75	80
Ser	Pro	Leu	Leu	Val	Gly	Pro	Val	Ser	Val	Ser	Phe	Ser	Pro	Val	Pro	85	90	95	
Ser	Leu	Ala	Glu	Ile	Val	Glu	Arg	Asn	Pro	Arg	Val	Glu	Pro	Gly	Gly	100	105	110	
Arg	Tyr	Arg	Pro	Ala	Gly	Cys	Glu	Pro	Arg	Ser	Arg	Thr	Ala	Ile	Ile	115	120	125	
Val	Pro	His	Arg	Ala	Arg	Glu	His	His	Leu	Arg	Leu	Leu	Leu	Tyr	His	130	135	140	
Leu	His	Pro	Phe	Leu	Gln	Arg	Gln	Gln	Leu	Ala	Tyr	Gly	Ile	Tyr	Val	145	150	155	160
Ile	His	Gln	Ala	Gly	Asn	Gly	Thr	Phe	Asn	Arg	Ala	Lys	Leu	Leu	Asn	165	170	175	
Val	Gly	Val	Arg	Glu	Ala	Leu	Arg	Asp	Glu	Glu	Trp	Asp	Cys	Leu	Phe	180	185	190	
Leu	His	Asp	Val	Asp	Leu	Leu	Pro	Glu	Asn	Asp	His	Asn	Leu	Tyr	Val	195	200	205	

Cys Asp Pro Arg Gly Pro Arg His Val Ala Val Ala Met Asn Lys Phe  
 210 215 220  
 Gly Tyr Ser Leu Pro Tyr Pro Gln Tyr Phe Gly Arg Val Ser Ala Leu  
 225 230 235 240  
 Thr Pro Asp Gln Tyr Leu Lys Met Asn Gly Phe Pro Asn Glu Tyr Trp  
 245 250 255  
 Gly Trp Gly Gly Glu Asp Asp Asp Leu Leu Pro Gly Cys Ala Trp Leu  
 260 265 270  
 Gly

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1686 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

AGATAAAGTA AGTGCTGTTT GGGCTAACAG GATCTCCTCT TGCACTCTGC AGCCCAGGAC	60
GCTGATTCCA GCAGCGCCTT ACCGCGCAGC CCGAAGATTC ACTATGGTGA AAATCGCCTT	120
CAATACCCCT ACCGCCGTGC AAAAGGAGGA GGCGCGGCAA GACGTGGAGG CCCTCCTGAG	180
CCGCACGGTC AGAACTCAGA TACTGACCGG CAAGGAGCTC CGAGTTGCCA CCCAGGAAAA	240
AGAGGGCTCC TCTGGGAGAT GTATGCTTAC TCTCTTAGGC CTTTCATTCA TCTTGGCAGG	300
ACTTATTGTT GGTGGAGCCT GCATTTACAA GTACTTCATG CCCAAGAGCA CCATTTACCG	360
TGGAGAGATG TKCTTTTTTG ATTCTGAGGA TCCTGCAAAT TCCCTTCGTG GAGGAGAGCC	420
TAACTTCCTG CCTGTGACTG AGGAGGCTGA CATTCGTGAG GATGACAACA TTGCAATCAT	480
TGATGTGCCT GTCCCCAGTT TCTCTGATAG TGACCCCTGCA GCAATTATTC ATGACTTTGA	540
AAAGGGAATG ACTGCTTACC TGGACTTGTT GCTGGGGAAC TGCTATCTGA TGCCCCTCAA	600
TACTTCTATT GTTATGCCTC CAAAAATCT GGTAGAGYTC TTTGGCAAAC TGGCGAGTGG	660
CAGATATCTG CYTCAAACCT ATGTGGTTCG AGAAGACCTA GTTGCTGTGG AGGAAATTCG	720
TGATGTTAGT AACCTTGGCA TCTTTATTTA CCAACTTTCG AATAACAGAA AGTCCTTCCG	780
CCTTCGTGCG AGAGACCTCT TGCTGGGTTT CAACAAACGT GCCATTGATA AATGCTGGAA	840

GATTAGACAC TTCCCCAACG AATTTATTGT TGAGACCAAG ATCTGTCAAG AGTAAGAGGC	900
AACAGATAGA GTGTCCTTGG TAATAAGAAG TCAGAGATTT ACAATATGAC TTTAACATTA	960
AGGTTTATGG GATACTCAAG ATATTTACTC ATGCATTTAC TCTATTGCTT ATGCTTTAAA	1020
AAAAGGAAAA GAAAAAACT ACTAACCACT GCAAGCTCTT GTCAAATTTT AGTTTAATTG	1080
GCATTGCTTG TTTTTGAAA CTGAAATTAC ATGAGTTTCA TTTTTCTTT GAATTTATAG	1140
GGTTTAGATT TCTGAAAGCA GCATGAATAT ATCACCTAAC ATCCTGACAA TAAATTCCAT	1200
CCGTTGTTTT TTTGTTTGT TTGTTTTTTC TTTTCCTTA AGTAAGCTCT TTATTCATCT	1260
TATGGTGCAG CAATTTTAAA ATTTGAAATA TTTTAAATTG TTTTGAAC TTTTGTGTAA	1320
AATATATCAG ATCTCAACAT TGTTGGTTTC TTTTGTTTT CATTTTGTAC AACTTTCTTG	1380
AATTTAGAAA TTACATCTTT GCAGTTCTGT TAGGTGCTCT GTAATTAACC TGACTTATAT	1440
GTGAACAATT TTCATGAGAC AGTCATTTTT AACTAATGCA GTGATTCTTT CTCACTACTA	1500
TCTGTATTGT GGAATGCACA AAATTGTGTA GGTGCTGAAT GCTGTAAGGA GTTTAGGTTG	1560
TATGAATTCT ACAACCCTAT AATAAATTTT ACTCTATAAA AAAAAAAAAA AAAAAAAAAA	1620
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	1680
AAAAAA	1686

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Met Val Lys Ile Ala Phe Asn Thr Pro Thr Ala Val Gln Lys Glu Glu	
1 5 10 15	
Ala Arg Gln Asp Val Glu Ala Leu Leu Ser Arg Thr Val Arg Thr Gln	
20 25 30	
Ile Leu Thr Gly Lys Glu Leu Arg Val Ala Thr Gln Glu Lys Glu Gly	
35 40 45	
Ser Ser Gly Arg Cys Met Leu Thr Leu Leu Gly Leu Ser Phe Ile Leu	
50 55 60	

Ala	Gly	Leu	Ile	Val	Gly	Gly	Ala	Cys	Ile	Tyr	Lys	Tyr	Phe	Met	Pro	65	70	75	80
Lys	Ser	Thr	Ile	Tyr	Arg	Gly	Glu	Met	Xaa	Phe	Phe	Asp	Ser	Glu	Asp	85	90	95	
Pro	Ala	Asn	Ser	Leu	Arg	Gly	Gly	Glu	Pro	Asn	Phe	Leu	Pro	Val	Thr	100	105	110	
Glu	Glu	Ala	Asp	Ile	Arg	Glu	Asp	Asp	Asn	Ile	Ala	Ile	Ile	Asp	Val	115	120	125	
Pro	Val	Pro	Ser	Phe	Ser	Asp	Ser	Asp	Pro	Ala	Ala	Ile	Ile	His	Asp	130	135	140	
Phe	Glu	Lys	Gly	Met	Thr	Ala	Tyr	Leu	Asp	Leu	Leu	Leu	Gly	Asn	Cys	145	150	155	160
Tyr	Leu	Met	Pro	Leu	Asn	Thr	Ser	Ile	Val	Met	Pro	Pro	Lys	Asn	Leu	165	170	175	
Val	Glu	Xaa	Phe	Gly	Lys	Leu	Ala	Ser	Gly	Arg	Tyr	Leu	Xaa	Gln	Thr	180	185	190	
Tyr	Val	Val	Arg	Glu	Asp	Leu	Val	Ala	Val	Glu	Glu	Ile	Arg	Asp	Val	195	200	205	
Ser	Asn	Leu	Gly	Ile	Phe	Ile	Tyr	Gln	Leu	Cys	Asn	Asn	Arg	Lys	Ser	210	215	220	
Phe	Arg	Leu	Arg	Arg	Arg	Asp	Leu	Leu	Leu	Gly	Phe	Asn	Lys	Arg	Ala	225	230	235	240
Ile	Asp	Lys	Cys	Trp	Lys	Ile	Arg	His	Phe	Pro	Asn	Glu	Phe	Ile	Val	245	250	255	
Glu	Thr	Lys	Ile	Cys	Gln	Glu	260												

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

TNCACATTCTC AGTGGGAACT TGATGAAC

29

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

ANATATAGGTG GAATGAATTC TATCCTTG

29

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

GNTATAGTAAT AATAGCACAA AGGACGGG

29

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

TNGCCAGGAAA CCAAATCAAT GACTCTTT

29

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

TNTAATTGACG GTGTAGAGAA ATGAGGAA

29

- (2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

ANAAATGGAGC AGCTGGGTGG AGGCAAGA

29

- (2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

TNCGGAGATAC TCCCAAGTCC AACAGTGA

29

- (2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GNTTAGGGCTT TCAGTAGCCC AGTTTCTC

29

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

ANTGACAGGTA CATCATGACA GCCAGCTG

29

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

CNGGATGTTAG GTGATATATT CATGCTGC

29

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 264 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Gly Glu Val Lys Ser Ser Gly Leu Leu Cys Arg Gly Thr Trp Ala Trp  
1 5 10 15

Ser Arg Leu Pro Arg Lys Cys Leu Cys Val Gln Ile Ser Arg His Leu  
20 25 30

Gly Lys Met Tyr Ser Glu Met Ile Phe Val Asn Gly Phe Val His Cys  
35 40 45

Asp Pro His Pro Gly Asn Val Leu Val Arg Lys His Pro Gly Thr Gly  
50 55 60

Lys Ala Glu Ile Val Leu Leu Asp His Gly Leu Tyr Gln Met Leu Thr  
65 70 75 80

Glu Glu Phe Arg Leu Asn Tyr Cys His Leu Trp Gln Ser Leu Ile Trp  
85 90 95

Thr Asp Arg Lys Arg Val Lys Glu Tyr Ser Gln Arg Leu Gly Ala Gly  
100 105 110

Asp Leu Tyr Pro Leu Phe Ala Cys Met Leu Thr Ala Arg Ser Trp Asp  
115 120 125

Ser Val Asn Arg Gly Ile Ser Gln Ala Pro Val Thr Ala Thr Glu Asp  
130 135 140

Leu Glu Ile Arg Asn Asn Ala Ala Asn Tyr Leu Pro Gln Ile Ser His  
145 150 155 160

Leu Leu Asn His Val Pro Arg Gln Met Leu Leu Ile Leu Lys Thr Asn  
165 170 175

Asp Leu Leu Arg Gly Ile Glu Ala Ala Leu Gly Thr Arg Ala Ser Ala  
180 185 190

Ser Ser Phe Leu Asn Met Ser Arg Cys Cys Ile Arg Ala Leu Ala Glu  
195 200 205

His Lys Lys Lys Asn Thr Cys Ser Phe Phe Arg Arg Thr Gln Ile Ser  
210 215 220

Phe Ser Glu Ala Phe Asn Leu Trp Gln Ile Asn Leu His Glu Leu Ile  
225 230 235 240

Leu Arg Val Lys Gly Leu Lys Leu Ala Asp Arg Val Leu Ala Leu Ile  
245 250 255

Cys Trp Leu Phe Pro Ala Pro Leu  
260



(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2355 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

CGCTTTTTTTT TTTTTTTTTT TTCAGAAGGA GGAAGCTCAT TATGTTTGGA TCACCCACAG 60  
CTATAGATTC TAAAAATATT TTGGCTTTTTT TTGAGGTGCT TTAGTAAAAT ATAACCCCAA 120  
ATGATTCACT TGGACAAGTG GTCTTAACAG CAAGGAAAAC AAACACTTTA TGAAAACAGC 180  
TATAAGCCTT CTGTCTTTTA TCTTTACTAT TTTCTCCGAG TCTGGCATGA AACAGATACA 240  
CAGCAGCCTC CACAGGGGGT TAAGTARAGA ACCATCCAAG CATCACAGAG TGTCATCCAG 300  
AATTCTGATG ACTTCCATTC GTTGACTCTG ATGCACAATA TGCCTGGCTT GGGATGCAGC 360  
GACCATGATG CCCCTCCCAG AACAGACACT TGCAGAGTGT TCCAGGAACA GCAGCTCCCT 420  
CCAGCCCCCA GCACAAGATG CACACATCTC AGAACAAGCC TCCATCCTTT TCCTAGAGAA 480  
CTGAGCATAA ATAAC TTGTT CTATATCTGG CTCCAAGTCC ATTTCTGTTC TGTCTTGAG 540  
TAGAGTCTTA GCTCCAGTT TGTTTTAGGT CAACTTTCAG CACCTACTTC AGCTCACTTG 600  
TTTGATTTAC TAAGCTCTTG CTTCTGTATA TTATCAAATG TAGGGATGTA GGGAGAATAA 660  
AAGGATCTAG ATACTTGCTT TTAGGAGAGA TTAGAACAAA GCTGAAGGTG GAGGCATTAG 720  
TTCCTAGGTC TTCAGATCTC AGAGCAAAGG ACCCACTCTG GAGCCTAAAT TCTATGAGAG 780  
ACCACAGAGC AGCCTGAAAT CCAAAGGAGT TTTACACAGG AAAAAAAAAA TACTGTGAGG 840  
ACTTACACTA AATAATAATG TTGTTTTGAA TGGGGTTGTG GGTAATTCCT ATATTCTTCT 900  
TTATAACTTT TGTACTTTTC AAATTCCCTA ATGTGAACTC ACTACTTAGT AGGTCTGTAA 960  
GCTTAAACAT TACTATGGCT TGGAATCTCA TTTCAAAAAA TCTTTAAAT GGGGACAAGA 1020  
GTAAAAATTT CTTAGCTTCT ATGGAAGAAT AAAATGAAAT TATAATGATA CAGTGCCTGG 1080  
CATGTTGTGG TCGCTCAATA AACACTGCTT TCCTCCCCAT TGTCTCCTC TTTATTCTGT 1140  
TTCATTACAA GGTGAGCAGA TTGAATCAGG ACCAGCTGGG AGGGCTACTT CTATGAGAGA 1200  
AGATCTGTCC ACAGTCATGG TTTTCAATGT TTAGTGCACC AGAATCACCT TGAGGGTTTG 1260  
TTAAACAGA CTGCTGAACA TAACACATCT ATGAGAATGG CAAAATCCA GAACACCAAA 1320  
TGCTGGTGAG GATGTGGAGC AATAAAAACT CTCATTTATT GCTGATGGCA ATGCAAAATG 1380

GTACAGCCAC TTTGGAAGAC AATTTGCCAA ATTTTACAA AACTAAGTGT ACTCTTACCA	1440
TACAATCTAG CAATCATGCT CCCTGGTATT TACCTAAAGG AGTTAAAAAC TTATGTCTAG	1500
ACAGAAACCT GCATATGAAT GTTTATAGCA GTTTTTTTTCA TAATTGCTAA ACTTTGGAAG	1560
TAACCAAGAT GCCCTTCAGC AGGTGAATGG ACAAATAAAC TGCAGTAGAT GCAGACAGTG	1620
GAATATCATT CTAGGCCATG AAGGCCGAAT TCGGCCTTCA TGGCCTAATT AAAGAAAGTC	1680
AGGATAAAAA TTTTAAAAAG CAGGCCACTG TCAGCAAAGC CTGGAGAAGT GGGGCCGGAG	1740
GYTCCGCCCC CATCATGTGC CTGCCACCCC TTCCCAGTCA TCCCTTTAYT CTTACAGTAG	1800
CAAATAAGAC CCCTGTCTAA TGGGGGGAGA CAAATGTGTA GACCCTTAGC CACCTTGGCC	1860
AGGGCTGACT CCTTAAATTT CTGGATGATG ATGATTGTTA TTTAATAGCC AGAGGCTCAT	1920
ATAATTGGCC TCTTTGGAAG AGGCCTCATG GCCTCCTTAC TCTCACCAA GCAATTTTTC	1980
CCTCAGGGGG GCTCCCATCT TCTTACACAG AGAGGCAGCT GAGGCAGGAC AGTGGGGCTA	2040
ACTGTAGACC AGGCGAGGGC ACGGGCTGCT GGGGTGGCCC TGCTTCCCCA GTGTACATAT	2100
TGTATCTGTG TAACATTTTG TATATTCCAG GGGTAGGGCC GCCCCCTGTA TCATACCTAG	2160
CAGAGGTTGG AGCTGGCACA TGGGGAGGAG GTTCTAATAA TTATTGGGG CTGGGAAACT	2220
TATTTATTGA TAGCATAGGA CAGAGGAAGG AGGCGGGGAT GGGGTCGTGG CGCCCTGGTG	2280
ATGCGACTCC TGTTTATTTT GCTTTTATT TCGGAATAAA TGGATTTAGC CATAAAAAAA	2340
AAAAAAAAAA AAAAA	2355

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Met	Lys	Thr	Ala	Ile	Ser	Leu	Leu	Ser	Phe	Ile	Phe	Thr	Ile	Phe	Ser
1				5					10					15	
Glu	Ser	Gly	Met	Lys	Gln	Ile	His	Ser	Ser	Leu	His	Arg	Gly	Leu	Ser
			20					25					30		
Xaa	Glu	Pro	Ser	Lys	His	His	Arg	Val	Ser	Ser	Arg	Ile	Leu	Met	Thr
			35				40					45			

Ser Ile Arg  
50

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2496 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

GCGCCCTTTC GGTCAACATC GTAGTCCACC CCCTCCCCAT CCCCAGCCCC CGGGGATTCA 60  
GGCTCGCCAG CGCCCAGCCA GGGAGCCGGC CGGGAAGCGC GATGGGGGCC CCAGCCGCCT 120  
CGCTCCTGCT CCTGCTCCTG CTGTTTCGCT GCTGCTGGGC GCCCGGCGGG GCCAACCTCT 180  
CCCAGGACGA CAGCCAGCCC TGGACATCTG ATGAAACAGT GGTGGCTGGT GGCACCGTGG 240  
TGCTCAAGTG CCAAGTGAAA GATCACGAGG ACTCATCCCT GCAATGGTCT AACCCCTGCTC 300  
AGCAGACTCT CTACTTTGGG GAGAAGAGAG CCCTTCGAGA TAATCGAATT CAGCTGGTTA 360  
CCTCTACGCC CCACGAGCTC AGCATCAGCA TCAGCAATGT GGCCCTGGCA GACGAGGGCG 420  
AGTACACCTG CTCAATCTTC ACTATGCCTG TGCGAACTGC CAAGTCCCTC GTCACTGTGC 480  
TAGGAATTCC ACAGAAGCCC ATCATCACTG GTTATAAATC TTCATTACGG GAAAAAGACA 540  
CAGCCACCCCT AAAGTGTGAG TCTTCTGGGA GCAAGCCTGC AGCCCGGCTC ACCTGGAGAA 600  
AGGGTGACCA AGAACTCCAC GGAGAACCAA CCCGCATACA GGAAGATCCC AATGGTAAAA 660  
CCTTCACTGT CAGCAGCTCG GTGACATTCC AGGTTACCCG GGAGGATGAT GGGGCGAGCA 720  
TCGTGTGCTC TGTGAACCAT GAATCTCTAA AGGGAGCTGA CAGATCCACC TCTCAACGCA 780  
TTGAAGTTTT ATACACACCA ACTGCGATGA TTAGGCCAGA CCCTCCCCAT CCTCGTGAGG 840  
GCCAGAAGCT GTTGCTACAC TGTGAGGGTC GCGGCAATCC AGTCCCCCAG CAGTACCTAT 900  
GGGAGAAGGA GGGCAGTGTG CCACCCCTGA AGATGACCCA GGAGAGTGCC CTGATCTTCC 960  
CTTTCCTCAA CAAGAGTGAC AGTGGCACCT ACGGCTGCAC AGCCACCAGC AACATGGGCA 1020  
GCTACAAGGC CTACTACACC CTCAATGTTA ATGACCCCAG TCCGGTGCCC TCCTCCTCCA 1080  
GCACCTACCA CGCCATCATC GGTGGGATCG TGGCTTTCAT TGTCTTCCTG CTGCTCATCA 1140  
TGCTCATCTT CCTCGGCCAC TACTTGATCC GGCACAAAGG AACCTACCTG ACACATGAGG 1200  
CAAAAGGCTC CGACGATGCT CCAGACGCGG ACACGGCCAT CATCAATGCA GAAGGCGGGC 1260

AGTCAGGAGG GGACGACAAG AAGGAATATT TCATCTAGAG GCGCCTGCCC ACTTCCTGCG	1320
CCCCCAGGG GCCCTGTGGG GACTGCTGGG GCCGTCACCA ACCCGGACTT GTACAGAGCA	1380
ACCGCAGGGC CGCCCCTCCC GCTTGCTCCC CAGCCCACCC ACCCCCCTGT ACAGAATGTC	1440
TGCTTTGGGT GCGGTTTTGT ACTCGGTTTG GAATGGGGAG GGAGGAGGGC GGGGGGAGGG	1500
GAGGGTTGCC CTCAGCCCTT TCCGTGGCTT CTCTGCATTT GGGTTATTAT TATTTTGTGA	1560
ACAATCCCAA ATCAAATCTG TCTCCAGGCT GGAGAGGCAG GAGCCCTGGG GTGAGAAAAG	1620
CAAAAAACAA ACAAAAAACA AAACCCTGGA GTGTTAGGAG GAGAGTGAAG GTAGAGGGGT	1680
GAGGAAGGGT AAGGGGCAGG GCTGGTTTCA GCTGGGGGCT CTCACCAGCC CTCCTTTCAG	1740
CCTCTACAAC AGAGCAGCTT CCCAGACTTC TCCAGGAACC CAGAAACGGG ATGGTTGTCTG	1800
GCAAAGGTTG GGAGTGGCTT TTCTCTGGT AGCCACACAC CTGAGCACTA CGGACAGGGA	1860
GGCAGGTGCC ACCTTGACAC CTCTCTTCCA TAGCAATGGG AAAGTGATGA GTGCGGGAGT	1920
CCTGAGGAGA TGTGGCCTGC AGACAACATG CAGCCATGCA GGGACCCAGG ACTGTAACTT	1980
GGGGAGGACG CGGGTCCCTG CAAGGAAGAG TAGATTTGGA GAGGAAGGAT GGAGGTGGAC	2040
TCTCACCCCA TTCCCCCGG AAATGAACAA AGCCGGGCCC TTTCCATAGG AACTGCCCTT	2100
GGAGATAGCA GAGTGTGGCT GCCCTCCTT GCTCCAGCAG CAGTGGGAGA GGCAGTCTC	2160
TGGGGCCTGA ACTGCCTCTG CTCCCCCCC TGAGGGGCCC CTCACTCTTA CCCAAGACTC	2220
TGGATTGTTG CACGGCAACC ACTCCTCCCA TGGCATTGCT CAGCAACTAC TTCTCCCTTC	2280
CCGGCCACCC TGTGCCCCCT TCCTGGTCCC AACGCCAGCC CTTCATCCTT CCTCCCTCAG	2340
CAGCCAGGCA GACATAACAA CAAACTACT AAAAGGAGCT TCAAAAAAAAA AAAAAAAAAA	2400
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	2460
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAA	2496

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

Met Gly Ala Pro Ala Ala Ser Leu Leu Leu Leu Leu Leu Phe Ala

1                      5                      10                      15  
 Cys Cys Trp Ala Pro Gly Gly Ala Asn Leu Ser Gln Asp Asp Ser Gln  
                          20                      25                      30  
 Pro Trp Thr Ser Asp Glu Thr Val Val Ala Gly Gly Thr Val Val Leu  
                          35                      40                      45  
 Lys Cys Gln Val Lys Asp His Glu Asp Ser Ser Leu Gln Trp Ser Asn  
                          50                      55                      60  
 Pro Ala Gln Gln Thr Leu Tyr Phe Gly Glu Lys Arg Ala Leu Arg Asp  
                          65                      70                      75                      80  
 Asn Arg Ile Gln Leu Val Thr Ser Thr Pro His Glu Leu Ser Ile Ser  
                          85                      90                      95  
 Ile Ser Asn Val Ala Leu Ala Asp Glu Gly Glu Tyr Thr Cys Ser Ile  
                          100                      105                      110  
 Phe Thr Met Pro Val Arg Thr Ala Lys Ser Leu Val Thr Val Leu Gly  
                          115                      120                      125  
 Ile Pro Gln Lys Pro Ile Ile Thr Gly Tyr Lys Ser Ser Leu Arg Glu  
                          130                      135                      140  
 Lys Asp Thr Ala Thr Leu Asn Cys Gln Ser Ser Gly Ser Lys Pro Ala  
                          145                      150                      155                      160  
 Ala Arg Leu Thr Trp Arg Lys Gly Asp Gln Glu Leu His Gly Glu Pro  
                          165                      170                      175  
 Thr Arg Ile Gln Glu Asp Pro Asn Gly Lys Thr Phe Thr Val Ser Ser  
                          180                      185                      190  
 Ser Val Thr Phe Gln Val Thr Arg Glu Asp Asp Gly Ala Ser Ile Val  
                          195                      200                      205  
 Cys Ser Val Asn His Glu Ser Leu Lys Gly Ala Asp Arg Ser Thr Ser  
                          210                      215                      220  
 Gln Arg Ile Glu Val Leu Tyr Thr Pro Thr Ala Met Ile Arg Pro Asp  
                          225                      230                      235                      240  
 Pro Pro His Pro Arg Glu Gly Gln Lys Leu Leu Leu His Cys Glu Gly  
                          245                      250                      255  
 Arg Gly Asn Pro Val Pro Gln Gln Tyr Leu Trp Glu Lys Glu Gly Ser  
                          260                      265                      270  
 Val Pro Pro Leu Lys Met Thr Gln Glu Ser Ala Leu Ile Phe Pro Phe  
                          275                      280                      285  
 Leu Asn Lys Ser Asp Ser Gly Thr Tyr Gly Cys Thr Ala Thr Ser Asn  
                          290                      295                      300  
 Met Gly Ser Tyr Lys Ala Tyr Tyr Thr Leu Asn Val Asn Asp Pro Ser

305		310		315		320
Pro Val Pro Ser Ser Ser Ser Thr Tyr His Ala Ile Ile Gly Gly Ile						
		325		330		335
Val Ala Phe Ile Val Phe Leu Leu Leu Ile Met Leu Ile Phe Leu Gly						
	340		345		350	
His Tyr Leu Ile Arg His Lys Gly Thr Tyr Leu Thr His Glu Ala Lys						
	355		360		365	
Gly Ser Asp Asp Ala Pro Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu						
	370		375		380	
Gly Gly Gln Ser Gly Gly Asp Asp Lys Lys Glu Tyr Phe Ile						
	385		390		395	

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2764 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GGGCCAAAGA GGCCTACCAG CTGCTGTTGA CCGCTGGACT CACAAACCTT TCTTTCTACT	60
CTTGTTTTTC ATTCACTTTG GGTCATTTTT CAGTGTGAT GGGGACGTAA TAAAGCACGG	120
TAAGAAAATC CGTGAATTCC GTCAGAGCAG TCGTCCAGAG GGAAGGCGCG CCCGGCGTAG	180
GGAGGTCAGA GCTCATGTTA GCTATGAACA CAGGTCACAG GGGCGTACGG CGATGGGAAA	240
CACTGAGATG CTCAATATAT TGATTATTTA ATAGTGTTTA GCAAAATGGT CTTTTTTTAT	300
TCCTTAAATC AACTGAAACT CACTTCACGT CTCTTCCTT GTAGAGCATC ATGCTTATTT	360
CTGGCTCACT CACATCTTTG TCTCGGGAGT TCTCTGCCGA GCCATTGCCC CCTACAGCAG	420
AGAGCACAGC TGGCTGCACT AGTGCTGAAG GAGCCAGCCC CAGAGCAGGG CATTTCCAGG	480
GGCTCTTGTC CCAGAGCGGC AGGCGTTGTG TGCAGAGAAC GCCCCTCCCA CGCAGCACAG	540
AGAACGCGGG GTGGGTGTGT GGCTCCGGGC CTGTGGGGCT TAGGCTGCCT GAACCACCGC	600
CGACTGGCAC CATGACTCGG CATTCTGGA AGTGCCTTAC CAAGTTGTTG TTGTTGTTTT	660
GTTGTTTTTT AAGAGACGGG CTTGCTCTAT CATCCAGGCT CGAGTGCAAT GGCACAGTCA	720
CAGCTCACTG CAGCCTTGAA CTCGTGGGCT CAAGCCATCC TCCTGTGTCA GCCTCCCCAG	780

TACCTGGGAC	TGTGGGCATG	AGCACTGCGC	CTGGCAGCTG	TATCAGTGTT	GACTCCACAT	840
TTTAATAGTT	GCTTCTTGAA	ATTAAAATGC	TTTGATTGAG	CCTTCAAGCC	ATCAGGAAAG	900
TTTGCCCCCTC	TGAGTCACAC	CTGGTGGTCT	CCAGGGTTCC	TGCCCCCTCCC	TCCTGAGCCA	960
GCTCCTCAGA	GCGGATAGAG	GCAGGACCCC	CACCCAGGTC	TTGAGACCCC	CCTGCCCCGC	1020
ACTCCCCCGG	AGACGGGCTA	CCCCTGCAGA	TGCAGATAGT	CAAAGCTCAG	GTTTCTTCCA	1080
AAGCTTTTAA	AAAGATATTG	TACCTTGAGC	ACTTTAAAAA	TGTCTTAAAA	TTGCCATACA	1140
GGCTCTTAAA	AGCTTATACG	TTTAAACTGT	TGATAGATGG	GCCTTTACTA	AAATGCATTC	1200
ATTTATTTTC	CTAATCCCTT	GGTTGTAAAA	TAATTCTGGG	GAAGGGCCCC	GAGCACGACA	1260
GCCGCAGTCT	CCACCCAGAA	CCAGAGAGTC	CCCCCAACC	CGGGATGTAC	CCTCTGGCCA	1320
CACCAGGGAC	CCTGCCAGAG	GCCGCAGACT	GGCAGCAGCA	GCCTCCCCAC	ACAGTGGGGG	1380
AAGGTCAGTG	TGATGCCTTC	AGGCCCCGTC	TCCTGCCAGG	GCTCTCCCTC	CAGCCTACAT	1440
AGGGCCTCAG	AGAAATGCAT	TTTTAGTTCT	GGCTTTGGCC	CAGCCCAGGG	CAAGGCAGGA	1500
AACTCTCCAG	CGTGAGTCCG	TGAGGGCCAA	GAAGTCCCGC	CCTGTTCTGG	GGGAGGACCT	1560
GGCTTTTCTG	GTGTCTCTGG	TGCCCCGAGAG	CCCGGTGCTG	CCATCTTTAG	TGAAAGAGTA	1620
AATGGTGGCC	GAGGGCTCCT	TTTGTGAGGG	ATGTGCCTTG	GTGAAGAAGG	CATGTTCCCT	1680
GCCGTGAAGA	TACTTGGAAG	CTCTGGGTGG	AGAGGGAAAA	GGGATACCCC	TGGTGCTCCC	1740
TGGGCCTGGC	GGAAGGCTAG	GAGGAAGGAC	AGCTGAGGTG	AGGACTGAGT	GGGGCAGGTA	1800
TCACCCTGAC	AAACAGTTTG	GGAAGATCAG	GAAAGGCAGG	TGAGACCTGG	TGCAGAATCC	1860
AGGTTGGGTA	ATAGATACAT	CGTCGAAGAT	GTAGCAAGCA	AAGTAATATA	CTCAACTCTG	1920
GAACATTGCA	CAGAAGCTTT	TAAAGCACTC	TGTGACACTT	TTTGTAATGA	GGGATCTGAA	1980
GGAAACGGCC	CCAGAGTCAC	CCATCCCCAC	GGGTCTGGTT	GGCGGGGCTG	GTGCCTTTCT	2040
TCTGCACTCA	GTCACCATGG	CTCCGTCTGT	CAAACCTAAC	TCTTTTTTTT	TTTTTTTTTTC	2100
TTCTCTTGGT	GTGGTAATTT	GTTTGAAGAG	CCACTCCATC	CCCAAATTCA	AGATTAGAAA	2160
GATCCCTGAC	TGCTTCTCAA	GATCCAGAAC	ATTCTTGAC	AGAGTATATT	CACCATTTAG	2220
AAGTGATCCA	GCAAAGATTG	GGAGGGGTAC	TACCAGATTC	TACTTCAAAG	AAATCCTGCC	2280
ACCCGATGAT	TAAACAGTGA	ATAAAATGTC	ATGGCTCTTT	CCTGCGACAA	TTCTATTTGA	2340
GGAAAAGATT	TGTTTTTCCC	TTTTCCCAAG	GAAGCTCGTG	GGACAGCATG	GGCACTACTC	2400
TTCATGTGCG	GTGACACCAG	CCCCCAGATG	CCTTGAATTA	AGTGTCTCTA	CCTTTATGCA	2460
TGACTGCAAA	GCCAGCTGGA	GCATTTTCTA	TGGAGCCTCC	GTATGTTTTA	GGCCCATGAC	2520

CTTCGTGAGG TGATGGGCAC TCACTCCCAT GAGCCCTGGC TGTGTGCTGT TGTGTGCCTA 2580  
TCGGCAGATC CATCCTTCCT GCCTCCAAGG AGGATACACA GAGAATGGCT TCCTGTTGTT 2640  
TTGTTTATTT TCTTAACGTG TACAGATGGA AACTTCATTT AAAAATAAAA ACAAACAAY 2700  
TCNAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 2760  
AAAA 2764

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

Met Leu Ile Ser Gly Ser Leu Thr Ser Leu Ser Arg Glu Phe Ser Ala  
1 5 10 15  
Glu Pro Leu Pro Pro Thr Ala Glu Ser Thr Ala Gly Cys Thr Ser Ala  
20 25 30  
Glu Gly Ala Ser Pro Arg Ala Gly His Phe Gln Gly Leu Leu Ser Gln  
35 40 45  
Ser Gly Arg Arg Cys Val Gln Arg Thr Pro Leu Pro Arg Ser Thr Glu  
50 55 60  
Asn Ala Gly Trp Val Cys Gly Ser Gly Pro Val Gly Leu Arg Leu Pro  
65 70 75 80  
Glu Pro Pro Pro Thr Gly Thr Met Thr Arg His Ser Trp Lys Cys Leu  
85 90 95  
Thr Lys Leu Leu Leu Leu Phe Cys Cys Phe Leu Arg Asp Gly Leu Ala  
100 105 110  
Leu Ser Ser Arg Leu Glu Cys Asn Gly Thr Val Thr Ala His Cys Ser  
115 120 125  
Leu Glu Leu Val Gly Ser Ser His Pro Pro Val Ser Ala Ser Pro Val  
130 135 140  
Pro Gly Thr Val Gly Met Ser Thr Ala Pro Gly Ser Cys Ile Ser Val  
145 150 155 160  
Asp Ser Thr Phe



(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3367 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

CAGAAGGGAG	GTAGTCGCCC	TCCGTCGTGG	CCTGGCGTGG	ATTCCGAGCG	TTGGTGTCTG	60
GCGGTTTCCG	ACCGTTGGTG	TCTGGCACGC	GCCACCCCGA	TGTACCAGGT	AAAGCCCTAT	120
CACGGGGTCG	GCGCCCCTCT	CCGTGTGGAG	CCCACCTGCA	TGTACTGGCT	CCCCAACATG	180
CACGGCAGGA	GCGGCGGCCC	AGCACTCGGC	ACTGGCCACT	TGCAGACAAG	AAGACAAGAA	240
AATGATTTGA	GGACAGCTTC	AATCGCGGTG	TGAAGAAGAA	AGCAACAAAA	CGACCACTGA	300
AAACAATGCC	GGTGGCAAAA	CATCCAAAGA	AAGGGTCCCA	AGCGGTACAT	CGTCATAGCT	360
GGAAACAGTC	AGAGCCACCA	GCCAATGATC	TTTTCAATGC	TGCGAAAGCT	GCCAAAAGTG	420
ACATGCAGTG	TGGCCATGAG	GTCTGCCGGA	AGTGACTTGT	TGGTGTATC	TCCTGAGTTA	480
AAATGTGAAG	GGATTTTTTT	TTTTCAGATT	ACTGAGAGTC	TTCTGTTACT	AGTTTGTCTT	540
TCCTAGATCC	AGACACGGGG	ACTGCAGAGA	AAGGCTGTGT	GCATCCGCTG	TCTACTCCAC	600
TGTCTCCTCT	GCAGAGGCGG	ATTTCCCTGA	CTGAAGACCA	TGTTGCAGGC	CCACAGCTGC	660
CTACAGAACC	GTCCCAAAAT	ATGGCAAAGA	AACCTATTCT	GAGGGTCTCA	CCATGTTGCC	720
CAGGCTGGTC	TTGAACTCCT	GGACTCATCC	TAAAGTGCTG	GCCTCTCATT	CCCTGTCTGT	780
GCACACCTCA	CGGCAAGGGC	CAGCCTGTTT	CCTCCCGGTC	ACCTCCAAAT	CTTGCTGCTT	840
TTAATTCAAC	TCAGAGGCCT	AGCCAGGGTT	GAGTTCTCAC	CCACCTGTGC	CGCCCTGCCT	900
TGTTACCTGG	AAGCACAGCC	TTGGGGACTG	AGCAGGCCCT	CACTGTCACT	TTAAGAAGGG	960
AATCAGCCAC	TTTGTGCTCA	CCACCTCTGG	GGAAGGTGTG	AGAGGAGAGA	AGGAAGTGGC	1020
TGTTTGGCTG	CTGACAACAT	GAAGACTTCC	TGCGATGAGA	ACAGAGGCAC	AGGTGCCGGC	1080
CCTGCAGCCC	CCAGAACCCG	GACTGGAGGG	GGCCATGGGG	CGCCGGACCC	TGGCCCTGCC	1140
CTGGGTGCTG	CTGACCCTGC	GTGTCACTGC	AGGGACCCCG	GAGGTGTGAG	TACAAGTTCTG	1200
GATGGAGGCC	ACCGAGCTCT	CGTCCTTCAC	CATCCGTTGT	GGGTTCTCTG	AGTCTGGCTC	1260
CATCTCCCTG	GTGACTGTGA	GCTGGGGGGG	CCCCGATGGT	GCTGGGGGGA	CCACGCTGGC	1320

TGTGTTGCAC	CCGGAACCTTG	GCATCCAGCA	ATGGGCCCCCT	GCTCGCCAGG	CCCGCTGGGA	1380
AACCCAGAGC	AGCGTCTCTC	TTGCCCTGGA	AGTCTCTGGG	GCCAGCAGCC	CCTGCACCAA	1440
CACCACCTTC	TGCTGCAAGT	TTGCGTCCTT	CCCTGAGGGC	TCCTGGGAGG	CCTCTGGGAG	1500
CCTCCCGCCC	AGCTCAGACC	CAGGGCTCTC	TGTCCCGCCG	ACTCCTGCCC	CCATTCTGCG	1560
GGCAGACCTG	GCCGGGATCT	TGGGGGTCTC	AGGAGTCCTT	CTCTTTGACT	GTGGCTACCT	1620
CCTTCATCTG	CTGTGCCGAC	AGAAGCACCG	CCCTGCCCCCT	AGGCTCCAGC	CATCCCACAC	1680
CAGCTCCTAG	GCACTGAGAG	CACGAGCATG	GGCACCCAGC	CAGGCCTCCC	AGGCTGCTCT	1740
CCACGTCCCT	TATGCCACTA	TCAACACCAG	CTGCTGCCCA	GCTACTTTGG	ACACAGCTCA	1800
CCCCCGACAG	GGGGCCGTCC	TGTCGTTTCC	TGCTGTGACT	AAGTCAGCAA	CACAGTTCCT	1860
CTGACATGGG	CCTTGGCTGT	GCTTCTTTGG	GGGTGAAGAG	ATTGGGGAGG	AAGTCTCCAC	1920
CCCTGGGAGG	CAGAAGCCAG	GCATAGCGCG	CTGGCTAGGA	CTCCAGTACC	GTGAAGGGAG	1980
GCAGTGAGAG	CAGACATCTG	TGTCTCATTC	CTGATCTCAA	GGGGAAAGCA	AGAACAAGGG	2040
AGGCTTCCTC	AGGATCTCAA	ACCTGCGGAA	GGAGGACCAG	TCTGTGTACT	TCTGCCAAGT	2100
CCAGCTGGAC	ATACAGATCA	GCCCTCAGGC	AGCCCCCTCA	CAGGACCCCT	CTCCTGCCTG	2160
GACAGCTCTG	CTGGTCTCCC	CGTCCCCTGG	AGAAGAACAA	GGCCATGGGT	CGGCCCCTGC	2220
TGCTGCCCCCT	GCTGCTCCTG	CTGCAGCCGC	CAGCATTTCT	GCAGCCTGGT	GGCTCCACAG	2280
GATCTGGTCC	AAGCTACCTT	TATGGGGTCA	CTCAACCAAA	ACACCTCTCA	GCCTCCATGG	2340
GTGGCTCTGT	GGAAATCCCC	TTCTCCTTCT	ATTACCCCTG	GGAGTTAGCC	ACAGCTCCCCG	2400
ACGTGAGAAT	ATCCTGGAGA	CGGGGCCACT	TCCACGGGCA	GTCCTTCTAC	AGCACAAGGC	2460
CGCCTTCCAT	TCACAAGGAT	TATGTGAACC	GGCTCTTTCT	GAACCTGGACA	GAGGGTCAGG	2520
AGAGCGGCTT	CCTCAGGATC	TCAAACCTGC	GGAAGGAGGA	CCAGTCTGTG	TATTTCTGCC	2580
GAGTCGAGCT	GGACACCCGG	AGATCAGGGA	GGCAGCAGTT	GCAGTCCATC	AAGGGGACCA	2640
AACTCACCAT	CACCCAGGCT	GTCACAACCA	CCACCACCTG	GACGCCCAGC	AGCACAACCA	2700
CCATAGCCGG	CCTCAGGGTC	ACAGAAAGCA	AAGGGCACTC	AGAATCATGG	CACCTAAGTC	2760
TGGACACTGC	CATCAGGGTT	GCATTGGCTG	TCGCTGTGCT	CAAACTGTG	ATTTTGGGAC	2820
TGCTGTGCCT	CCTCCTGTGG	TGGAGGAGAA	GGAAAGGTAG	CAGGGCGCCA	AGCAGTGACT	2880
TCTGACCAAC	AGAGTGTGGG	GAGAAGGGAT	GTGTATTAGC	CCCGGAGGAC	GTGATGTGAG	2940
ACCCGCTTGT	GAGTCCTCCA	CACTCGTTCC	CCATTGGCAA	GATACATGGA	GAGCACCTG	3000

AGGACCTTTA AAAGGCAAAG CCGCAAGGCA GAAGGAGGCT GGGTCCCTGA ATCACCGACT 3060  
GGAGGAGAGT TACCTACAAG AGCCTTCATC CAGGAGCATC CACACTGCAA TGATATAGGA 3120  
WTGAGGTCTG AACTCCACTG AATTAAACCA CTGGCATTTC GGGGCTGTTC ATTATAGCAG 3180  
TGCAAAGAGT TCCTTTATCC TCCCCAAGGA TGGAAAATAC AATTTATTTT GCTTACCATA 3240  
CACCCCTTTT CTCTTCGTCC ACATTTTCCA ATCTGTATGG TGGCTGTCTT CTATGGCAGA 3300  
AGGTTTTGGG GAATAAATAG CGTGAAATGC TAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 3360  
AAAAAAA 3367

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

Met Gly Arg Pro Leu Leu Pro Leu Leu Leu Leu Gln Pro Pro  
1 5 10 15  
Ala Phe Leu Gln Pro Gly Gly Ser Thr Gly Ser Gly Pro Ser Tyr Leu  
20 25 30  
Tyr Gly Val Thr Gln Pro Lys His Leu Ser Ala Ser Met Gly Gly Ser  
35 40 45  
Val Glu Ile Pro Phe Ser Phe Tyr Tyr Pro Trp Glu Leu Ala Thr Ala  
50 55 60  
Pro Asp Val Arg Ile Ser Trp Arg Arg Gly His Phe His Gly Gln Ser  
65 70 75 80  
Phe Tyr Ser Thr Arg Pro Pro Ser Ile His Lys Asp Tyr Val Asn Arg  
85 90 95  
Leu Phe Leu Asn Trp Thr Glu Gly Gln Glu Ser Gly Phe Leu Arg Ile  
100 105 110  
Ser Asn Leu Arg Lys Glu Asp Gln Ser Val Tyr Phe Cys Arg Val Glu  
115 120 125  
Leu Asp Thr Arg Arg Ser Gly Arg Gln Gln Leu Gln Ser Ile Lys Gly  
130 135 140  
Thr Lys Leu Thr Ile Thr Gln Ala Val Thr Thr Thr Thr Trp Thr  
145 150 155 160

Pro Ser Ser Thr Thr Thr Ile Ala Gly Leu Arg Val Thr Glu Ser Lys  
165 170 175

Gly His Ser Glu Ser Trp His Leu Ser Leu Asp Thr Ala Ile Arg Val  
180 185 190

Ala Leu Ala Val Ala Val Leu Lys Thr Val Ile Leu Gly Leu Leu Cys  
195 200 205

Leu Leu Leu Trp Trp Arg Arg Arg Lys Gly Ser Arg Ala Pro Ser Ser  
210 215 220

Asp Phe  
225

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3899 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

GGGAAGAGAT GGTGACTGAG GCAGAAGCTA ATAGGGAAGA TGATAGGAAA GAAATTTTAC	60
CCAAGGGAAT TAGATTTAGC AAGAGAGCGA AGGAAAGCTG AGAGGCCAAA AACATCTCTG	120
AGGAAAACTG ACTCTGAGAG AGAAGAGGTG ACAAGGGCAA ATGCACTCAA GGATGAAGAT	180
GCTTTTAAAG AAGAGCAAAA ACTTAAAGCG GAAGAAGGGG AAACAGAGAC AGAAGTWAGA	240
GCTGAGGAAG AGACAAAAGC TCCCCCAAAT GAAATGGGAT CTGATGCTGA RAACGAASCA	300
CCTGTGGAGG CTTCTGAGTT GTCTGACAAT CCAGGGCTTC TAGGAGAARA TTCTACTAAA	360
GAGACAGTGG TTCCCATATT TGAAGCAACG CCTGGATTTG AAAAGTCGCT GGAAAACATA	420
ACAGCTCTGA GGAAAGAAGG AGGAGGGGAA AGACTGAGTG AAGCCAGAGA CACAGAGCAC	480
AAAGACAGAG AAGAGCTGTC CAGCAGGGAG AATAGGGCCC TGAAGGAAGG GCACCGCCAA	540
GATGGAGAGG GGGCCTTAGC AGCTCCTGAA GCTGAGCCAG CAGGAAAGGT GCAGGCCCCCT	600
GAGGGGCTGA TCCCAGCCAC AGGCCAGGCA GAGGAGCTAG CAGCCAAAGA TCACGACTCC	660
TGCGCAGGAC TGGAGGGGAG AGCTGAAGGG CAAGGAGGAG TGGATGTCGT GCTAAGGACC	720
CAGGAAGCTG TTGCTGAGGA AGATCCCATA WTGGCAGAAA AGTTCAGGGA GGAAGCGGTG	780
GATGAGGACC CAGAGGAGGA AGAGGACAAA GAGTGCAATC TGGAGACAGA AGCGATGCAG	840

GACAGGAACT CGGAAGGGGA CGGGGACATG GAAGGAGAAG GAAACACACA AAAGAATGAG 900  
 GGCATGGGAG GAGGAAGGGT TGTGGCTGTG GAAGTTCTAC ACGGAGGTGG TGAAACGGCA 960  
 GAAACAGCCG CAGAGGAGAG GGAGGTGTTG GCAGGTTTCGG AGACAGCCGA GGAGAAAACA 1020  
 ATAGCAAATA AAGCCTCCTC CTTTTCAGAT GTTGCTGAGG AAGAAACCTG GCACCAACAG 1080  
 GATGAGTTAG TAGGAAAAAC AGCAGCTGCA GGAAGGTGG TGGTAGAGGA ATTAGCACGG 1140  
 AGTGGGGAGG AAGTGCCAGC AGCAGAGGAG ATGACAGTGA CATATACAAC AGAGGCTGGG 1200  
 GTGGGCACTC CAGGAGCCCT GGAGCGGAAG ACCTCAGGGC TAGGACAGGA GCAAGAGGAA 1260  
 GGGTCAGAGG GCCAGGAGGC AGCCACTGGG AGTGGCGATG GGAGGCAGGA GACAGGAGCA 1320  
 GCTGAAAAAT TCCGATTAGG ATTATCACGG GAGGGAGAGA GGAATTGAG TCCGGAGAGT 1380  
 CTACAGGCGA TGGCAACACT TCCAGTGAAG CCTGATTTCA CTGAAACCCG AGAGAAGCAA 1440  
 CAGCATATGG TGCAAGGAGA AAGCGAGACT GCAGATGTTT CCCCCAACAA CATGCAGGTC 1500  
 TAGGAGACTT GCTGGCAGAC GGATAATTTA AAGATGTCTT CTGAAGATGT AAAGAGTGGA 1560  
 GAAAGATTCA CGCAAGCATC TCACCAGGAT TCTTGATTTT CTCTCTCTCC TCTTTAGTTG 1620  
 CTGGTTGCGC TTGTCTGAGA TGATTCCCAA TCTGTCAGCC CTGGTCAGTA GCTCAGTAAG 1680  
 CACCTTGAGA ATAGCTCAAG TAGATCTGTA GGACCCCTCT TAGAAGCAGT GGTTCCCTCAT 1740  
 GGAGAACTT GTGAGGCTGT TACACATTCT ACACACCTAA CATTATTTTC AAACAAAAT 1800  
 GATAATTTTC AGATGCTTGA CTTTACCAA AGATCACTGG AAGGCCAGT CCTAATGTTA 1860  
 GGGGTTTGTT TAAAGTCCTT TTTATTTTAC AATACAGAGC CCCAGTCAAT TCCACAATCT 1920  
 CAATTTTATA CATGGGAATT TTATTTAAAA ATCTGTGGTT TGGGGCTTTA ATGAATTGGC 1980  
 CTGTGAAAAT GAGCTCTAAA TTTCTCCCA CGTACACTCA AACTCAAGA TTGCTCCAAA 2040  
 TCTCTAAGTT CTTCCAGCAA AAGATTTCTT GGCATGTATA TTCACTTATA CTTAGAAATA 2100  
 TTCATTCTTT TAATTTATGC CAGAATAACA AAGTGGAAT CTTATTTCAA AATGCTCTTT 2160  
 GTTTTTTTGT GTGTGTTTCT GTAGTTCTGC TTTCTGGGGT AGACTAGTAA AATGGTAGCT 2220  
 TCCAGCATTT TGTCCCTGGG GCCTTCTTTA TAGGGCCACT CAAATTTAAA TAAAGTAGT 2280  
 AAATAATTTA GCTAAGTGGA ATAAGTATAA TAATTATAGT GGTAAGCATA GCACATCAGC 2340  
 ATTATGCCAA CATTCTAGAC TCTTTAGTTG ATGTCATTAA ATGGAAAAGA AACTTGGAAT 2400  
 AAATGAGTGT GCTGCTCACC TTCCCAAGTT CTGTTATTTT AAACCTGTGA ACTAACCTTG 2460  
 CAGTTCATTA TAAATCAACA GTAACAACCTG CATTCTAAAT TACTCCCTGA TATTATTTTC 2520

TAGTTGTGTA TCAGCCTGTC TCCTAGGGGT TTTCAATTTCC CTGAAGACAT ACAAGTGCCC	2580
CAGAGCGCAT GTATATGTCT ACCATTTCTC TATATGAGAA GGTAACAAAAA ATTTCTTTAA	2640
GCAGTGATTT TCCAGCCAGA ATATACATTA GATTTTCATG GGACGCTTTT ATAAATGACT	2700
CAACCCTTTT CCCCACCCCA GAGATTCAGA CTTAATTCGT TTTAGATGGA TCTACACATC	2760
AGTATATATA TATTTTAAAC TTTTCACTTG ATTCTTCTCT GTAGCCAAGG TTGAGAACCG	2820
CTGTTCTAAA TCATCATATA ATCCATGCTG GCCACATTAC ACTCAAGGTC CCTAGGGACC	2880
AGGCATATTA TCATAGTAGG TATCTTCCAT TTTAATGTGT AATGGAGCCA TTCAATGATC	2940
AAAAATACAC TGGACCAGAT AGTAGACTGG TCCCTTGATC AGAAGCATCA GCACATCAGC	3000
ATCACCTGGA AATTGTTCCC AGCCTTTGTC TCCTACCTAC TAAATTAGAA ACTCTTGGTG	3060
GGTTCCAGTA ATCCATAGCT TAACAAGCCC TGCAGTTAAT ACTGATGTAC ACTGATGTCC	3120
AAAAACTGCT GTCATGGACT ATTGATTGTA TTGAGGATTA GTCTCAGTTG GAAAGCCAAC	3180
TACAGAGGCA TTTTGAACCT TCTTTCTTTG CCTCTCTATG TCTCTCTGTC TTTTCTGTCT	3240
TTCTGATTTA TCTGTCTTTC TTTCTCTAGT AAATGGCACT CAATATAAAA GTGGTGGAGT	3300
CAATCTTAAA CTTATTTTAA TTATGATTGT ATTGATACAT GCACGAAGTC CCTCTGCCCT	3360
ACTCCCTATT CAAGGATATT ACTCACTGCA CATCATAAAT CTCCATCATC TGTCTTAAAG	3420
TTTTATGAGT AGATTTTCATC TACATTATAT TCAAGTTCAT TTATTACTGA GCTGTATTAC	3480
TGTGGAGCTC TAACAGTATT TGTTTCCTGA TTTCAAACCTC AATGCTACAG AGCACTTTGA	3540
ATACATCACA CCTTATAGGA AAGATAGTAA ATGTATTAAT CCCATTGAAA AATTAGTTTT	3600
GTACAATGTG CTAAATAGTA TTGCATTGGA TTACTTTTAT ATTTAACACA CTCCATCAAA	3660
ACATCCCATA ACATAATTTT ACAATCTGCA TGTGAATTTA ACTGTGAAAT TCAGTATTGT	3720
GATATTTTGA ATAAGTGAAT TCTTTCTCTG CAAATACTAT GTTGATAAAA TTACTTGTAT	3780
GTTCCCCTGA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	3840
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAGA	3899

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

Met	Ile	Gly	Lys	Lys	Phe	Tyr	Pro	Arg	Glu	Leu	Asp	Leu	Ala	Arg	Glu	
1				5					10					15		
Arg	Arg	Lys	Ala	Glu	Arg	Pro	Lys	Thr	Ser	Leu	Arg	Lys	Thr	Asp	Ser	
			20					25					30			
Glu	Arg	Glu	Glu	Val	Thr	Arg	Ala	Asn	Ala	Leu	Lys	Asp	Glu	Asp	Ala	
		35					40					45				
Phe	Lys	Glu	Glu	Gln	Lys	Leu	Lys	Ala	Glu	Glu	Gly	Glu	Thr	Glu	Thr	
	50					55					60					
Glu	Val	Arg	Ala	Glu	Glu	Glu	Thr	Lys	Ala	Pro	Pro	Asn	Glu	Met	Gly	
65					70					75					80	
Ser	Asp	Ala	Glu	Asn	Glu	Xaa	Pro	Val	Glu	Ala	Ser	Glu	Leu	Ser	Asp	
				85					90					95		
Asn	Pro	Gly	Leu	Leu	Gly	Glu	Xaa	Ser	Leu	Lys	Glu	Thr	Val	Val	Pro	
			100					105						110		
Ile	Phe	Glu	Ala	Thr	Pro	Gly	Phe	Glu	Lys	Ser	Leu	Glu	Asn	Ile	Thr	
		115					120					125				
Ala	Leu	Arg	Lys	Glu	Gly	Gly	Gly	Glu	Arg	Leu	Ser	Glu	Ala	Arg	Asp	
	130					135					140					
Thr	Glu	His	Lys	Asp	Arg	Glu	Glu	Leu	Ser	Ser	Arg	Glu	Asn	Arg	Ala	
145					150					155					160	
Leu	Lys	Glu	Gly	His	Arg	Gln	Asp	Gly	Glu	Gly	Ala	Leu	Ala	Ala	Pro	
				165					170					175		
Glu	Ala	Glu	Pro	Ala	Gly	Lys	Val	Gln	Ala	Pro	Glu	Gly	Leu	Ile	Pro	
			180						185				190			
Ala	Thr	Gly	Gln	Ala	Glu	Glu	Leu	Ala	Ala	Lys	Asp	His	Asp	Ser	Cys	
		195					200					205				
Ala	Gly	Leu	Glu	Gly	Arg	Ala	Glu	Gly	Gln	Gly	Gly	Val	Asp	Val	Val	
	210					215					220					
Leu	Arg	Thr	Gln	Glu	Ala	Val	Ala	Glu	Glu	Asp	Pro	Ile	Xaa	Ala	Glu	
225					230					235					240	
Lys	Phe	Arg	Glu	Glu	Ala	Val	Asp	Glu	Asp	Pro	Glu	Glu	Glu	Glu	Asp	
				245					250					255		
Lys	Glu	Cys	Xaa	Leu	Glu	Thr	Glu	Ala	Met	Gln	Asp	Arg	Asn	Ser	Glu	
			260					265					270			
Gly	Asp	Gly	Asp	Met	Glu	Gly	Glu	Gly	Asn	Thr	Gln	Lys	Asn	Glu	Gly	
		275					280					285				

Met Gly Gly Gly Arg Val Val Ala Val Glu Val Leu His Gly Gly Gly  
290 295 300

Glu Thr Ala Glu Thr Ala Ala Glu Glu Arg Glu Val Leu Ala Gly Ser  
305 310 315 320

Glu Thr Ala Glu Glu Lys Thr Ile Ala Asn Lys Ala Ser Ser Phe Ser  
325 330 335

Asp Val Ala Glu Glu Glu Thr Trp His Gln Gln Asp Glu Leu Val Gly  
340 345 350

Lys Thr Ala Ala Ala Gly Lys Val Val Val Glu Glu Leu Ala Arg Ser  
355 360 365

Gly Glu Glu Val Pro Ala Ala Glu Glu Met Thr Val Thr Tyr Thr Thr  
370 375 380

Glu Ala Gly Val Gly Thr Pro Gly Ala Leu Glu Arg Lys Thr Ser Gly  
385 390 395 400

Leu Gly Gln Glu Gln Glu Glu Gly Ser Glu Gly Gln Glu Ala Ala Thr  
405 410 415

Gly Ser Gly Asp Gly Arg Gln Glu Thr Gly Ala Ala Glu Lys Phe Arg  
420 425 430

Leu Gly Leu Ser Arg Glu Gly Glu Arg Glu Leu Ser Pro Glu Ser Leu  
435 440 445

Gln Ala Met Ala Thr Leu Pro Val Lys Pro Asp Phe Thr Glu Thr Arg  
450 455 460

Glu Lys Gln Gln His Met Val Gln Gly Glu Ser Glu Thr Ala Asp Val  
465 470 475 480

Ser Pro Asn Asn Met Gln Val  
485

(2) INFORMATION FOR SEQ ID NO:109:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 483 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

CATTGCTAGA CAGACTCTCT TGCTTGGATG GTACTCCACC ACTTTCTTGG CACATGAGAT 60  
GCAAGATTGC TCAGGGTGCA GCTAATGGCA TCAATTTTCT ACATGAAAAT CATCATATTC 120



ATAGAGATAT TAAAAGTGCA AATATCTTAC TGGATGAAGC TTTTACTGCT AAAATATCTG 180  
 ACTTTGGCCT TGCACGGGCT TCTGAGAAGT TTTGCCCAGA CAGTCATGAC TAGCAGAATT 240  
 GTGGGAACAA CAGCTTATAT GGCACCAGAA GCTTTGCGTG GAGAAATAAC ACCCAAATCT 300  
 GATATTTACA GCTTTGGTGT GGTTTTACTA GAAATAATAA CTGGACTTCC AGCTGTGGAT 360  
 GAACACCGTG AACCTCAGTT ATTGCTAGAT ATTAAAGAAG AAATTGAAGA TGAAGAAAAG 420  
 ACATTGAAGA TTATATTGAT AAAAAGATGA ATGATGCTGA TTCCACTTCA GTTGAAGCTA 480  
 TGT 483

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Met Ala Ser Ile Phe Tyr Met Lys Ile Ile Ile Phe Ile Glu Ile Leu  
 1 5 10 15  
 Lys Val Gln Ile Ser Tyr Trp Met Lys Leu Leu Leu Leu Lys Tyr Leu  
 20 25 30  
 Thr Leu Ala Leu His Gly Leu Leu Arg Ser Phe Ala Gln Thr Val Met  
 35 40 45  
 Thr Ser Arg Ile Val Gly Thr Thr Ala Tyr Met Ala Pro Glu Ala Leu  
 50 55 60  
 Arg Gly Glu Ile Thr Pro Lys Ser Asp Ile Tyr Ser Phe Gly Val Val  
 65 70 75 80  
 Leu Leu Glu Ile Ile Thr Gly Leu Pro Ala Val Asp Glu His Arg Glu  
 85 90 95  
 Pro Gln Leu Leu Leu Asp Ile Lys Glu Glu Ile Glu Asp Glu Glu Lys  
 100 105 110  
 Thr Leu Lys Ile Ile Leu Ile Lys Arg  
 115 120

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 493 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

AATCTGAGTC AGCTTAGAAG ATANTCCAAG CTCAGATGA TAACCACAGC CTGGGCTGAC	60
ACCTGGATTT CAGCTTTGCA TGATCCTCAG TATGAGAATC TATCTGTTCT GTGCTGGACT	120
TCTAATATAT AGAACTGTGA GATAATGGGT CACATTGGCT GGATGTGGTG GCTCATACCT	180
GTAAATCCCA GCACTTTGGG AGGCCGAGGC AGGCAGATCA CCTGAGGTCA GGAGTTCAAG	240
ACCGGCCTGG CCAGCATGGT GAAGCCCCGT CTTTACTAGA AATACAAAAA TTAGACGAGC	300
GTGGTGGTGG ACACCTGTGT TCCCAGCTAC TTGGGAGGCT GAGGCAGGAG ACTGGCTGGA	360
ACCAGGGAGG TAGAGGTTGC AGTGAGCTGA GATCGTGCCA CTGCACTCCA GCCTGGGTGA	420
CAGAGTGAGA CTCCATCATA AATAAATAAA TAAATAAATG GGTACATTA AGCCTTTAAA	480
AAAAAAAAAA AAA	493

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2682 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

GGTTCCAGAG AGAGTTTGCG ACGTGGTAAA GAAATAAGGC GAGTACACAA GCGAAGACTT	60
TCCAGCTCAG AGAGTGAAGA GAGCTATTTG TCCAAGAACT CTGAAGATGA TGAGCTAGCT	120
AAAGAATCAA AGCGGTCAGT TCGAAAGCGG GGCCGAAGCA CAGACGAGTA TTCAGAAGCA	180
GATGAGGAGG AGGAGGAAGA RGAAGGCAAA CCATCCCGCA AACGGCTACA CCGGATTGAG	240
ACGGATGAGG ARGAGAGTTG TGACAATGCT CATGGAGATG CAAATCAGCC TGCCCGTGAC	300
AGCCAGCCTA GGGTCCTGCC CTCAGAACAA GAGAGCACCA AGAAGCCCTA CCGGATAGAA	360
AGTGATGAGG AAGAGGACTT TGAAAATGTA GGCAAAGTGG GGAGCCCATT GGA CTATAGC	420
TTAGTGGACT TACCTTCAAC CAATGGACAG AGCCCTGGCA AAGCCATTGA GAACTTGATT	480

GGCAAGCCTA	CTGAGAAGTC	TCAGACCCCC	AAGGACAACA	GCACAGCCAG	TGCAAGCCTA	540
GCYTCCCAAT	GGGACAAGTG	GTGGGCAGGA	GGCAGGAGCA	CCAGAAGAGG	AGGAAGATGA	600
GCTTTTGAGA	GTGACTGACC	TTGTTGATTA	TGTCTGTAAC	AGTGAACAGT	TATAAGACTT	660
TTTTTCCATT	TTTGTGCTAA	TTTATTCCAC	GGTAGCTCTC	ACACCAGCGG	GCCAGTTATT	720
AAAAGCTGTT	TAATTTTTTC	TAGAAAACCTC	CACTACAGAA	TGACTTTTAG	AAGAAAAATT	780
TCAACAAATC	CTGAAGTCTT	TCTGTGAAGT	GACCAGTTCT	GAACCTTGAA	GATAAATAAT	840
TGCTGTAAAT	TCCTTTTGAT	TTTCTTTTTC	CAGGTTCATG	GTCCTTGGTA	ATTTCAATTCA	900
TGGAAAAAAA	TCTTATTATA	ATAACAACAA	AGATTTGTAT	ATTTTTGACT	TTATATTTCC	960
TGAGCTCTCC	TGACTTTGTG	AAAAAGGGTG	ATGAAAATGC	ATTCCGAATC	TGTGAGGGCC	1020
CAAAACAGAA	TTTAGGGGTG	GGTGAAAGCA	CTTGTGCTTT	AGCTTTTTCA	TATTAAATAT	1080
ATATTATATT	TAAACATTCA	TGGCATAGAT	GATGATTTAC	AGACAATTTA	AAAGTTCAAG	1140
TCTGTACTGT	TACAGTTTGA	GAATTGTAGA	TAACATCATA	CATAAGTCAT	TTAGTAACAG	1200
CCTTTGTGAA	ATGAACCTGT	TTACTATTGG	AGATAACCAC	ACTTAATAAA	GAAGAGACAG	1260
TGAAAGTACC	ATCATAATTA	ACCTAAATTT	TTGTTATAGC	AGAGTTTCTT	GTTTAAAAAA	1320
AAAWAAAAG	CRKCYGMAAA	GCATTTGTAC	AGTAAAATGT	ATAATGAAGC	TTTGCCAACC	1380
AGACTGTGCT	AGCAACAAAT	TTTTTTAAAT	AAGCTTTATG	CAGTGGAAT	AAGGTGGCCT	1440
CAAATATATT	GTGTCTGATG	GAGAGTTATT	AGTGAAATGA	ATGTGGTCTT	TCTTAAGGCC	1500
TGGGTGGACT	GTAAACTTTG	CCAATAGTAT	AACCTCTGTC	TTCTGGCCAC	TTGATGTTTA	1560
AATATCTGAA	ATATCATTTT	GAAAAAATA	CATCTATATA	TAACATACAT	GAAGAGATGC	1620
TAAGCTGACA	GTGATATTTT	AGCACATTTG	AAGACTGGGA	AGAGATTTTC	AGGTGAATTT	1680
TAAGTGGTCT	ATTCTTGCCC	TTAGTATCTA	CTTCAAATTG	AAGTCTACAA	ACAAAGCAGT	1740
TCCTTTGGGA	GGTTTTTAGT	TTGAGTTTTA	GCGTGTGTGT	GTGTTTGTGT	GTGTGCGTGT	1800
GCGTGTGTGT	GTGTGTTGGA	ATTTCCATATC	TGCCTGGATA	TATTAGCAGA	GTTTGAATGT	1860
AGTTTTGGCC	TTTGGCCATT	AGACTTCTAT	TAAAATTCAT	TAATAGTCAT	ACAACCAACA	1920
TAGAGTTGAA	TGAGAACTGC	CGATGTAATT	AATAGGCATG	ACATCCATTT	CAAACATCTC	1980
AACACTTTAA	AGAAAAGCCC	TTTGTTCCTCA	GAAAAAAGGG	TTTGTAACCTA	ACTAAATACC	2040
TAACATGTAA	TTGACACTAA	AATATGAACT	TTGTCTTATT	TAGTTTCTGT	TATAGCTGTA	2100
AAATTTACAG	CAGAGCCATA	ACATTGTACA	GAGTGTAGCA	CTTGTGATTA	AACCTAGCCT	2160
GTTAAATCCT	GAAACCTTCA	ACCATTACTT	CTGTGAATAC	TTTAGCCCTG	GGATTTGGGT	2220

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TTTTCTGTTC CGGTGTTGTG TCTGTTGCCG GCAATGGACA CACCATATCT GCTGCTGGCC      2280
CAAGGAACGT CATTAATTTT TCTTTCCAAA TTAAGTATTA TGTGCTAGTC AGTGTATAGT      2340
AAAGCACTTC TCTTTTTTAT TACTAAAAAG CTGGCATTAG ATTTGCATTA TAAATACCTC      2400
TCTAGGAACT TTATACTCCT TTTCCTTCTT CAACAGGTAT TGCCCTTAAA TCTTATCTTT      2460
TGGCCTTGAA AGTTTATAGC TATTGTTTTT CAGTTGTTCG TTGTTTGTGTT TTGTTTCACT      2520
TTAGTTCTGT AGTACCTGCC CATTAATATT TTTGCTTTGA TTCTAGCAAT GTGTATGTAT      2580
CTGTATAAAA AATAAATAA TGAAAGCAAC CTAAAAATAG GATGCACCAA TTAAAAA      2640
AAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AA                               2682

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(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 58 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

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Met Glu Lys Asn Leu Ile Ile Ile Thr Thr Lys Ile Cys Ile Phe Leu
 1                   5                   10                   15
Thr Leu Tyr Phe Leu Ser Ser Pro Asp Phe Val Lys Lys Gly Asp Glu
                20                   25                   30
Asn Ala Phe Arg Ile Cys Glu Gly Pro Lys Gln Asn Leu Gly Val Gly
          35                   40                   45
Glu Ser Thr Cys Ala Leu Ala Phe Ser Tyr
 50                   55

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(2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2522 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

GCCGAGCGCC CGCGCCGCCG CTGCCTCTGT CCTCCGCGCG CTGCTCAGCT GAAGGCGCAC	60
AGGATTCAAT TACTGGACTT GTCAACTCTG CCAGTGTACG TGCCATTTCT CTTCCACTAT	120
GAGAGGACCG ATTGTATTGC ACATTGTCTT GGCTTTCTGT AGCCTTCTGC TTTTCAGCGT	180
TGCCACACAA TGTCTGGCCT TCCCCAAAAT AGAAAGGAGG AGGGAGATAG CACATGTTCA	240
TGCGGAAAAA GGGCAGTCCG ATAAGATGAA CACCGATGAC CTAGAAAATA GCTCTGTTAC	300
CTCAAAGCAG ACTCCCCAAC TGGTGGTCTC TGAAGATCCA ATGATGATGT CAGCAGTACC	360
ATCGGCAACA TCATTAAATA AAGCATTCTC GATTAACAAA GAAACCCAGC CTGGACAAGC	420
TGGGCTCATG CAAACAGAAC GCCCTGGTGT TTCCACACYT ACTGAGTCAG GTGTCCCCTC	480
AGCTGAAGAA GTATTTGGTT CCAGCCAGCC AGAGAGAATA TCTCCTGAAA GTGGACTTGC	540
CAAGGCCATG TTAACCATG CTATCACTGC GACTCCTTCT CTGACTGTTG ATGAAAAGGA	600
GGAACCTCCTT ACAAGCACTA ACTTTCAGCC CATTGTAGAA GAGATCACAG AAACCACAAA	660
AGGTTTTCTG AAGTATATGG ATAATCAATC ATTTGCAACT GAAAGTCAGG AAGGAGTTGG	720
TTTGGGACAT TCACCTTCAT CCTATGTGAA TACTAAGGAA ATGCTAACCA CCAATCCAAA	780
GACTGAGAAA TTTGAAGCAG ACACAGACCA CAGGACAAC TCTTTTCCTG GTGCTGAGTC	840
CACAGCAGGC AGTGAGCCTG GAAGCCTCAC CCCTGATAAG GAGAAGCCTT CGCAGATGAC	900
AGCTGATAAC ACCCAGGCTG CTGCCACCAA GCAACCACTC GAAACTTCCG AGTACACCCT	960
GAGTGTGAG CCAGAACTG ATAGTCTGCT GGGAGCCCCA GAAGTCACAG TGAGTGTCAG	1020
CACAGCTGTT CCAGCTGCCT CTGCCTTAAG TGATGAGTGG GATGACACCA AATTAGAGAG	1080
TGTAAGCCGG ATAAGGACCC CCAAGCTTGG AGACAATGAA GAGACTCAGG TGAGAACGGA	1140
GATGTCTCAG ACAGCACAAG TAAGCCATGA GGGTATGGAA GGAGGCCAGC CTTGGACAGA	1200
GGCTGCACAG GTGGCTCTGG GGCTGCCTGA AGGGGAAACA CACACGGGCA CAGCCCTGCT	1260
AATAGCGCAT GGAATGAGA GATCACCTGC TTTCCTGAT CAAAGTTCCT TTACCCCCAC	1320
AAGTCTGATG GAAGACATGA AAGTTTCCAT TGTGAACTTG CTCCAAAGTA CGGGAGACTT	1380
CACGGAATCC ACCAAGGAAA ACGATGCCCT GTTTTTCTTA GAAACCACTG TTTCTGTCTC	1440
TGTATATGAG TCTGAGGCAG ACCAACTGTT GGGAAATACA ATGAAAGACA TCATCACTCA	1500
AGAGATGACA ACAGCTGTTC AAGAGCCAGA TGCCACTTTA TCCATGGTGA CACAAGAGCA	1560
GGTTGCTACC CTCGAGCTTA TCAGAGACAG TGGCAAGACT GAGGAAGAAA AGGAGGACCC	1620
CTCTCCTGTG TCTGACGTTT CTGGTGTAC TCAGCTGTCA AGAAGATGGG AGCCTCTGGC	1680
CACTACAATT TCAACTACAG TCGTCCCTTT GTCTTTTGAA GTTACTCCCA CTGTGGAAGA	1740

ACAAATGGAC ACAGTCACAG GGCCAAATGA GGAGTTCACA CCAGTTCCTGG GATCTCCAGT 1800  
 GACACCTCCT GGAATAATGG TGGGGGAACC CAGCATTTCC CCTGCACTTC CTGCTTTGGA 1860  
 GGCATCCTCT GAGAGAAGAA CTGTTGTTCC ATCTATTACT CGTGTTAATA CAGCTGCCTC 1920  
 ATATGGCCTG GACCAACTTG AATCTGAAGA GGGACAAGAA GATGAGGATG AAGAGGATGA 1980  
 AGAAGATGAA GATGAAGAAG AGGAAGATGA GGAAGAAGAT GAGGAAGATA AAGATGCAGA 2040  
 CTCGCTGGAT GAGGGCTTGG ATGGTGACAC TGAGCTGCCA GGTTTTACCC TCCCTGGTAT 2100  
 CACATCCCAG GAACCAGGCT TAGAGGAGGG AAACATGGAC CTGTTGGAGG GAGCTACCTA 2160  
 CCAGGTGCCA GATGCCYTCG AGTGGAACA GCAGAATCAA GGCCTGGTGA GAAGCTGGAT 2220  
 GGAAAAATM AAAGACAAGG CTGGTTACAT GTCTGGGATG CTGGTGCCTG TAGGGGTTGG 2280  
 GATAGCTGGA GCCTTGTTCA TCTTGGGAGC CCTCTACAGC ATTAAGGTTA TGAATCGCCG 2340  
 AAGGAGAAAT GGCTTCAAAA GGCATAAAAG AAAGCAGAGA GAATTCAACA GCATGCAAGA 2400  
 TCGAGTAATG CTCTTAGCCG ACAGCTCTGA AGATGAATTT TGAATTGGAC TGGGTTTTAA 2460  
 TTGGGATATT CAACGATGCT ACTATTCTAA TTTTATTTT GGAGCAGAAA AAAAAAAAAA 2520  
 AA 2522

(2) INFORMATION FOR SEQ ID NO:115:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 774 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

Met	Arg	Gly	Pro	Ile	Val	Leu	His	Ile	Cys	Leu	Ala	Phe	Cys	Ser	Leu
1					5				10					15	
Leu	Leu	Phe	Ser	Val	Ala	Thr	Gln	Cys	Leu	Ala	Phe	Pro	Lys	Ile	Glu
			20					25					30		
Arg	Arg	Arg	Glu	Ile	Ala	His	Val	His	Ala	Glu	Lys	Gly	Gln	Ser	Asp
		35					40					45			
Lys	Met	Asn	Thr	Asp	Asp	Leu	Glu	Asn	Ser	Ser	Val	Thr	Ser	Lys	Gln
	50					55					60				
Thr	Pro	Gln	Leu	Val	Val	Ser	Glu	Asp	Pro	Met	Met	Ser	Ala	Val	
65						70				75				80	

Pro Ser Ala Thr Ser Leu Asn Lys Ala Phe Ser Ile Asn Lys Glu Thr  
 85 90 95  
 Gln Pro Gly Gln Ala Gly Leu Met Gln Thr Glu Arg Pro Gly Val Ser  
 100 105 110  
 Thr Xaa Thr Glu Ser Gly Val Pro Ser Ala Glu Glu Val Phe Gly Ser  
 115 120 125  
 Ser Gln Pro Glu Arg Ile Ser Pro Glu Ser Gly Leu Ala Lys Ala Met  
 130 135 140  
 Leu Thr Ile Ala Ile Thr Ala Thr Pro Ser Leu Thr Val Asp Glu Lys  
 145 150 155 160  
 Glu Glu Leu Leu Thr Ser Thr Asn Phe Gln Pro Ile Val Glu Glu Ile  
 165 170 175  
 Thr Glu Thr Thr Lys Gly Phe Leu Lys Tyr Met Asp Asn Gln Ser Phe  
 180 185 190  
 Ala Thr Glu Ser Gln Glu Gly Val Gly Leu Gly His Ser Pro Ser Ser  
 195 200 205  
 Tyr Val Asn Thr Lys Glu Met Leu Thr Thr Asn Pro Lys Thr Glu Lys  
 210 215 220  
 Phe Glu Ala Asp Thr Asp His Arg Thr Thr Ser Phe Pro Gly Ala Glu  
 225 230 235 240  
 Ser Thr Ala Gly Ser Glu Pro Gly Ser Leu Thr Pro Asp Lys Glu Lys  
 245 250 255  
 Pro Ser Gln Met Thr Ala Asp Asn Thr Gln Ala Ala Ala Thr Lys Gln  
 260 265 270  
 Pro Leu Glu Thr Ser Glu Tyr Thr Leu Ser Val Glu Pro Glu Thr Asp  
 275 280 285  
 Ser Leu Leu Gly Ala Pro Glu Val Thr Val Ser Val Ser Thr Ala Val  
 290 295 300  
 Pro Ala Ala Ser Ala Leu Ser Asp Glu Trp Asp Asp Thr Lys Leu Glu  
 305 310 315 320  
 Ser Val Ser Arg Ile Arg Thr Pro Lys Leu Gly Asp Asn Glu Glu Thr  
 325 330 335  
 Gln Val Arg Thr Glu Met Ser Gln Thr Ala Gln Val Ser His Glu Gly  
 340 345 350  
 Met Glu Gly Gly Gln Pro Trp Thr Glu Ala Ala Gln Val Ala Leu Gly  
 355 360 365  
 Leu Pro Glu Gly Glu Thr His Thr Gly Thr Ala Leu Leu Ile Ala His  
 370 375 380

Gly Asn Glu Arg Ser Pro Ala Phe Thr Asp Gln Ser Ser Phe Thr Pro  
 385 390 395 400  
 Thr Ser Leu Met Glu Asp Met Lys Val Ser Ile Val Asn Leu Leu Gln  
 405 410 415  
 Ser Thr Gly Asp Phe Thr Glu Ser Thr Lys Glu Asn Asp Ala Leu Phe  
 420 425 430  
 Phe Leu Glu Thr Thr Val Ser Val Ser Val Tyr Glu Ser Glu Ala Asp  
 435 440 445  
 Gln Leu Leu Gly Asn Thr Met Lys Asp Ile Ile Thr Gln Glu Met Thr  
 450 455 460  
 Thr Ala Val Gln Glu Pro Asp Ala Thr Leu Ser Met Val Thr Gln Glu  
 465 470 475 480  
 Gln Val Ala Thr Leu Glu Leu Ile Arg Asp Ser Gly Lys Thr Glu Glu  
 485 490 495  
 Glu Lys Glu Asp Pro Ser Pro Val Ser Asp Val Pro Gly Val Thr Gln  
 500 505 510  
 Leu Ser Arg Arg Trp Glu Pro Leu Ala Thr Thr Ile Ser Thr Thr Val  
 515 520 525  
 Val Pro Leu Ser Phe Glu Val Thr Pro Thr Val Glu Glu Gln Met Asp  
 530 535 540  
 Thr Val Thr Gly Pro Asn Glu Glu Phe Thr Pro Val Leu Gly Ser Pro  
 545 550 555 560  
 Val Thr Pro Pro Gly Ile Met Val Gly Glu Pro Ser Ile Ser Pro Ala  
 565 570 575  
 Leu Pro Ala Leu Glu Ala Ser Ser Glu Arg Arg Thr Val Val Pro Ser  
 580 585 590  
 Ile Thr Arg Val Asn Thr Ala Ala Ser Tyr Gly Leu Asp Gln Leu Glu  
 595 600 605  
 Ser Glu Glu Gly Gln Glu Asp Glu Asp Glu Glu Asp Glu Glu Asp Glu  
 610 615 620  
 Asp Glu Glu Glu Glu Asp Glu Glu Glu Asp Glu Glu Asp Lys Asp Ala  
 625 630 635 640  
 Asp Ser Leu Asp Glu Gly Leu Asp Gly Asp Thr Glu Leu Pro Gly Phe  
 645 650 655  
 Thr Leu Pro Gly Ile Thr Ser Gln Glu Pro Gly Leu Glu Glu Gly Asn  
 660 665 670  
 Met Asp Leu Leu Glu Gly Ala Thr Tyr Gln Val Pro Asp Ala Xaa Glu  
 675 680 685



Trp Glu Gln Gln Asn Gln Gly Leu Val Arg Ser Trp Met Glu Lys Xaa  
 690 695 700  
 Lys Asp Lys Ala Gly Tyr Met Ser Gly Met Leu Val Pro Val Gly Val  
 705 710 715 720  
 Gly Ile Ala Gly Ala Leu Phe Ile Leu Gly Ala Leu Tyr Ser Ile Lys  
 725 730 735  
 Val Met Asn Arg Arg Arg Arg Asn Gly Phe Lys Arg His Lys Arg Lys  
 740 745 750  
 Gln Arg Glu Phe Asn Ser Met Gln Asp Arg Val Met Leu Leu Ala Asp  
 755 760 765  
 Ser Ser Glu Asp Glu Phe  
 770

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2002 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

GGCAGCCCGG TACCTGAAGT CCTTCAGAAAG TGACAGCCCGG GACCAGGATT CCGGGAGGCC	60
GACTCCTCCC TGCCCCACGA ATGCCGGGAA TTGTGGTCTC CGCCGGACGC GAGTTGTGAG	120
ACGGCCCAAG GGGCCGCGGG GTATGCTGGG ACCGCTAGCC CTTCCGGCGC GCCTCAGGAC	180
TTCGGGTCCC CTCACCCCGG GCGGATGCCC AAAGACTCCG CCTTCCCAAG AGCCCCTGCG	240
GCCGGGCGCG AAAATGGCGG CGGCGGCGAC GGCCGGGCGC TCCTGAAGCA GCAGTTATGG	300
AGCTTCCCTC AGGGCCGGGG CCGGAGCGGC TCTTTGACTC GCACCGGCTT CCGGGTGACT	360
GCTTCCTACT GCTCGTGCTG CTGCTCTACG CGCCAGTCGG GTTCTGCCTC CTCGTCCTGC	420
GCCTGTTTCT CGGGATCCAC GTCTTCCTGG TCAGCTGCGC GCTGCCAGAC AGCGTCCTTC	480
GCAGATTTCGT AGTGCGGACC ATGTGTGCGG TGCTAGGGCT CGTGGCCCGG CAGGAGGACT	540
CCGGACTCCG GGATCACAGT GTCAGGGTCC TCATTTCCAA CCATGTGACA CCTTTCGACC	600
ACAACATAGT CAATTTGCTT ACCACCTGTA GCACCGTGAG TGAGAGCGAG GCCGAGAGCG	660
CCACGGGGCG GTTCCCTGGG GCCCAGCTGA AGGCCCCCCT GTCCCCACTC GCGTTCCCCA	720
TGGAGGATAC TGAGCCTTAC CCCTAACCCC GATCCTCTAC CCAACATGTC AGTTTTTTTT	780

TTCATTTTCC TCAATATTTT TCTTCTTGCT TTCTCTTCTC CTGGTTCCCA GCCTCTACTC	840
AATAGTCCCC CCAGCTTTGT GTGCTGGTCT CGGGGCTTCA TGGAGATGAA TGGGCGGGGG	900
GAGTTGGTGG AGTCACTCAA GAGATTCTGT GCTTCCACGA GGCTTCCCCC CACTCCTCTG	960
CTGCTATTCC CTGAGGAAGA GGCCACCAAT GGCCGGGAGG GGCTCCTGCG CTTCAGAGTT	1020
TGACAGTTGC CTGTTATAAG GCAGGTGTGA GCTGCTGACT AGGCTGGCTG GATTCCCATC	1080
CTACTTTCTC CTTCTCTTTC TAGTTCCTGG CCATTTTCTA TCCAAGATGT GGTACAACCT	1140
CTTACCCTGC AAGTTCAGAG ACCCCTGGTC TCTGTGACGG TGTCAGATGC CTCCTGGGTC	1200
TCAGAACTGC TGTGGTCACT TTTCGTCCCT TTCACGGTGT ATCAAGTGGC TTCGTCTGT	1260
TCATCGCCAA CTAGGGGAAG CGAATGAGGA GTTTGCACTC CGTGTACAAC AGCTGGTGGC	1320
CAAGGAATTG GGCCAGACAG GGACACGGCT CACTCCAGCT GACAAAGCAG AGCACATGAA	1380
GCGACAAAGA CACCCCAGAT TGCGCCCCCA GTCAGCCCAG TCTTCTTTCC CTCCCTCCCC	1440
TGGTCCTTCT CCTGATGTGC AACTGGCAAC TCTGGCTCAG AGAGTCAAGG AAGTTTTGCC	1500
CCATGTGCCA TTTGGTGTCA TCCAGAGAGA CCTGGCCAAG ACTGGCTGTG TAGACTTGAC	1560
TATCACTAAT CTGCTTGAGG GGGCCGTAGC TTTCATGCCT GAAGACATCA CCAAGGGAAC	1620
TCAGTCCCTA CCCACAGCCT CTGCCTCCAA GTTTCCCAGC TCTGGCCCCG TGACCCCTCA	1680
GCCAACAGCC CTAACATTTG CCAAGTCTTC CTGGGCCCCG CAGGAGAGCC TGCAGGAGCG	1740
CAAGCAAGCA CTATATGAAT ACGCAAGAAG GAGATTCACA GAGAGACGAG CCCAGGAGGC	1800
TGACTGAGCT CAAAGGAACA GGATGGCACC CAGAGCCGCA GGACGGAGAC TGGGGGCAGC	1860
CCTCACCCAA CTCACAACAG GCTGGATGGG TGGGTGGTAA AAAGGGAAGG ATGAGGCTCC	1920
CCCAATGTCA CATTAAATTC ATGGTTTTCA TTCAAGGVAA AAAAAAAAAA AAAAAAAAAA	1980
AAAAAAAAAA AAAAAAAAAA AA	2002

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

Met	Pro	Pro	Gly	Ser	Gln	Asn	Cys	Cys	Gly	His	Phe	Ser	Ser	Leu	Ser	1	5	10	15
Arg	Cys	Ile	Lys	Trp	Leu	Arg	Pro	Val	His	Arg	Gln	Leu	Gly	Glu	Ala	20	25	30	
Asn	Glu	Glu	Phe	Ala	Leu	Arg	Val	Gln	Gln	Leu	Val	Ala	Lys	Glu	Leu	35	40	45	
Gly	Gln	Thr	Gly	Thr	Arg	Leu	Thr	Pro	Ala	Asp	Lys	Ala	Glu	His	Met	50	55	60	
Lys	Arg	Gln	Arg	His	Pro	Arg	Leu	Arg	Pro	Gln	Ser	Ala	Gln	Ser	Ser	65	70	75	80
Phe	Pro	Pro	Ser	Pro	Gly	Pro	Ser	Pro	Asp	Val	Gln	Leu	Ala	Thr	Leu	85	90	95	
Ala	Gln	Arg	Val	Lys	Glu	Val	Leu	Pro	His	Val	Pro	Phe	Gly	Val	Ile	100	105	110	
Gln	Arg	Asp	Leu	Ala	Lys	Thr	Gly	Cys	Val	Asp	Leu	Thr	Ile	Thr	Asn	115	120	125	
Leu	Leu	Glu	Gly	Ala	Val	Ala	Phe	Met	Pro	Glu	Asp	Ile	Thr	Lys	Gly	130	135	140	
Thr	Gln	Ser	Leu	Pro	Thr	Ala	Ser	Ala	Ser	Lys	Phe	Pro	Ser	Ser	Gly	145	150	155	160
Pro	Val	Thr	Pro	Gln	Pro	Thr	Ala	Leu	Thr	Phe	Ala	Lys	Ser	Ser	Trp	165	170	175	
Ala	Arg	Gln	Glu	Ser	Leu	Gln	Glu	Arg	Lys	Gln	Ala	Leu	Tyr	Glu	Tyr	180	185	190	
Ala	Arg	Arg	Arg	Phe	Thr	Glu	Arg	Arg	Ala	Gln	Glu	Ala	Asp	195	200	205			

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

CAATTGGGCC GCGAGTTGTG GTTTAAACCA GGAGTGC GCC GCGTCCGTTC ACCGCGGCCT	60
CAGATGAATG CGGCTGT TAA GACCTGCAAT AATCCAGAAT GGCTACTCTG ATCTATGTTG	120
ATAAGGAAAA TGGAGAACCA GGCACCCGTG TGGTTGCTAA GGATGGGCTG AAGCTGGGGT	180

CTGGACCTTC AATCAAAGCC TTAGATGGGA GATCTCAAGT TTCAACACCA CGTTTTGGCA	240
AAACGTTCTGA TGCCCCACCA GCCTTACCTA AAGCTACTAG AAAGGCTTTG GGAAGTGTCA	300
ACAGAGCTAC AGAAAAGTCT GTAAAGACCA AGGGACCCCT CAAACAAAAA CAGCCAAGCT	360
TTTCTGCCAA AAAGATGACT GAGAAGACTG TTAAAGCAAA AAGCTCTGTT CCTGCCTCAG	420
ATGATGCCTA TCCAGAAATA GAAAAATTCT TTCCCTTCAA TCCTCTAGAC TTTGAGAGTT	480
TTGACCTGCC TGAAGAGCAC CAGATTGCGC ACCTCCCCTT GAGTGGAGTG CCTCTCWTGA	540
TCCTTGACGA GGAGAGAGAG CTTGAAAAGC TGTTTCAGCT GGGCCCCCCT TCACCTGTGA	600
AGATGCCCTC TCCACCATGG GAATCCAATC TGTTGCAGTC TCCTTCAAGC ATTCTGTCTGA	660
CCCTGGATGT TGAATTGCCA CCTGTTTGCT GTGACATAGA TATTTAAATT TCTTAGTGCT	720
TCAGAGTTTG TGTGTATTTG TATTAATAAA GCATTCTTTA ACAGAAAAAA AAAAAAAAAA	780
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	819

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

Met	Ala	Thr	Leu	Ile	Tyr	Val	Asp	Lys	Glu	Asn	Gly	Glu	Pro	Gly	Thr
1			5					10					15		
Arg	Val	Val	Ala	Lys	Asp	Gly	Leu	Lys	Leu	Gly	Ser	Gly	Pro	Ser	Ile
			20					25					30		
Lys	Ala	Leu	Asp	Gly	Arg	Ser	Gln	Val	Ser	Thr	Pro	Arg	Phe	Gly	Lys
			35				40					45			
Thr	Phe	Asp	Ala	Pro	Pro	Ala	Leu	Pro	Lys	Ala	Thr	Arg	Lys	Ala	Leu
	50					55				60					
Gly	Thr	Val	Asn	Arg	Ala	Thr	Glu	Lys	Ser	Val	Lys	Thr	Lys	Gly	Pro
65				70					75					80	
Leu	Lys	Gln	Lys	Gln	Pro	Ser	Phe	Ser	Ala	Lys	Lys	Met	Thr	Glu	Lys
			85					90						95	
Thr	Val	Lys	Ala	Lys	Ser	Ser	Val	Pro	Ala	Ser	Asp	Asp	Ala	Tyr	Pro

100	105	110
Glu Ile Glu Lys Phe Phe Pro Phe Asn Pro Leu Asp Phe Glu Ser Phe		
115	120	125
Asp Leu Pro Glu Glu His Gln Ile Ala His Leu Pro Leu Ser Gly Val		
130	135	140
Pro Leu		
145		

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

TNTCCTGCCTC AGCTGCCTCT CTGTGTAA

29

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

CNCACTGCCCT CTTTCTCCCA TAGGTACT

29

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

GNAATAAGCAT GATGCTCTAC AAGGAAAG

29

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

TNGGTGCCATG ATTCTGAGTG CCCTTTGC

29

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

GNATATGTCAC TGTCATCTCC TCTGCTGC

29

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

ANAAGCTTCAT CCAGTAAGAT ATTTGCAC

29

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

ANTTCAGAACT GGTCACCTCA CAGAAAGA

29

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

GNATTCACATA GGATGAAGGT GAATGTCC

29

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

ANTAGAGGCTG GGAACCAGGA GAAGAGAA

29

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

TNTTGCAGGTC TTAACAGCCG CATTTCATC

29

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 113 amino acids  
(B) TYPE: amino acid

(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Met Glu Leu Pro Ser Gly Pro Gly Pro Glu Arg Leu Phe Asp Ser His  
1                               5                               10                               15  
Arg Leu Pro Gly Asp Cys Phe Leu Leu Leu Val Leu Leu Leu Tyr Ala  
                              20                               25                               30  
Pro Val Gly Phe Cys Leu Leu Val Leu Arg Leu Phe Leu Gly Ile His  
                              35                               40                               45  
Val Phe Leu Val Ser Cys Ala Leu Pro Asp Ser Val Leu Arg Arg Phe  
                              50                               55                               60  
Val Val Arg Thr Met Cys Ala Val Leu Gly Leu Val Ala Arg Gln Glu  
65                               70                               75                               80  
Asp Ser Gly Leu Arg Asp His Ser Val Arg Val Leu Ile Ser Asn His  
                              85                               90                               95  
Val Thr Pro Phe Asp His Asn Ile Val Asn Leu Leu Thr Thr Cys Ser  
                              100                               105                               110  
Thr

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 63 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

Ser Gln Pro Leu Leu Asn Ser Pro Pro Ser Phe Val Cys Trp Ser Arg  
1                               5                               10                               15  
Gly Phe Met Glu Met Asn Gly Arg Gly Glu Leu Val Glu Ser Leu Lys  
                              20                               25                               30  
Arg Phe Cys Ala Ser Thr Arg Leu Pro Pro Thr Pro Leu Leu Leu Phe  
                              35                               40                               45  
Pro Glu Glu Glu Ala Thr Asn Gly Arg Glu Gly Leu Leu Arg Phe  
                              50                               55                               60



(2) INFORMATION FOR SEQ ID NO:132:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 49 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Ser Ser Trp Pro Phe Ser Ile Gln Asp Val Val Gln Pro Leu Thr Leu  
1                    5                    10                    15  
  
Gln Val Gln Arg Pro Leu Val Ser Val Thr Val Ser Asp Ala Ser Trp  
                    20                    25                    30  
  
Val Ser Glu Leu Leu Trp Ser Leu Phe Val Pro Phe Thr Val Tyr Gln  
                    35                    40                    45  
  
Val

(2) INFORMATION FOR SEQ ID NO:133:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 2754 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

CAGGTGGTCC TCCACCTGCC TTGGCTTCCT AAAGTGCTGG GATTACAGGC ATGAGTCACT 60  
CTGCTGGCCT ATGTTCTGTT TTTGTTTTTTG TTTTGTGTTT GAGACAGAGT TTCACTCTTG 120  
TTGCCCAGGC TGGAGTGCAA TGGCATAATC TCGGCTCACT GCAGCCTCTG CCTCCCAGGT 180  
TCAAGTGATT CTCCTGCCTC AGCCTCCTGA GTAGCTGGGA TTACAGGCAT GTGCCACCTC 240  
ACCTGGCTAA TTTTGTATTT TTAGTAGAGA TGGGGTTTCT CCATGTTAGT CAGGCTGGTC 300  
TTGAACTCCT GACCTCAGGT GATCTGCCCT CCTCAGCCTC CTAAAGTGCT GGGATTACAG 360  
GTGTGAGCCA CTGTGCCCAG CCTTGTTTTT TGTTTTTTTG TTTTGTGTTT TTTTTTTGAC 420  
AGTAGCCATC CTAATAGATA CTAAGTGGTA TCTCATTGTG GTTTTGATTG CATGCGTTCT 480  
TTTTGGCTTG TTTTTTGAGA CAAGGTCTCA CTCCATCACC CAGACTGGAG CGCAGTGGTG 540  
TGATCACGGC TCGTTGCAAC CTGACCCTCT TGAGCTCAGG TGATCCTCCC ACTTCACCCT 600  
CCCGAGTATC TTGGAGTACA GGTGTGTGCC TGGCTGATTT TTCGTATTTT TTGTAGAGAT 660

GGGGTTTCAC	CGTGTGCTC	AGGCTGCTCT	CAAACCTGCTG	GGCTCAAACG	ATCCTCCTGC	720
CTTGGCCTCC	CAAAGTGCTG	GGGTTACAAG	CATGAACCAT	TATGCCCGGC	CTGCATGCAC	780
TCTTACACAC	GTTTTATCTG	TTACATATCC	CAAGATGTGT	AGTTCTTTGG	GAAGCAGGAA	840
GAAATGGGGG	TAACATTGAG	AAGTTAAGGA	AAACTGGTAT	AAATTATTGG	CAGCAGCTCC	900
TGATTATAGG	TTTTGAGGCC	TGAGTCCATG	GGCAGAGTCC	CTCTCCTGCA	GTTTCATGAGA	960
TTTGTACCCT	CCAGTGACAG	TACTGGGAAG	GAGGGAATGC	TACGTTCCAA	CTCTTAGTCT	1020
TCACTTAATT	TTATGACTCA	AAATTCCAGC	TAGATATATA	GGTTACTTTT	ACTGTTGGAT	1080
CACTCTGGCC	CACGAATGTA	TCCTGCTAAC	TTGATGTGTG	CTCTAACTAC	CTCCTAAGTT	1140
TGGTGACAGT	CGGCAGAGTT	TGTGAACCAT	GTGATTCCCA	ACTTAAGTTA	CTAACATTTT	1200
TTTTTTTTTT	TTTTGAGACA	GGATCTTGCT	CTGTCACCCA	GGCTGGAGTG	CAGTGGTACG	1260
ATCTCAGCTC	ACTGTAGCCT	TAACCCACCC	AGGCTTATGT	GCTCCTCCCA	CCTCAGCCTC	1320
CCGAGTAGTT	GGAACATAG	GTGCATACCA	CCATGCCTGG	CTAATTTTGT	TATTTTTTGT	1380
AGAGGCAGGG	TTTTGCCCTG	TTGCCCAGGC	TGGTCTTGAA	CTCCTGAGCT	CAAGCAATCC	1440
TCCCACCTCA	GCCTCCCAA	GGGTTGGGAT	TACAGGTGTG	AGCCACTGCA	CCCGGCCAAG	1500
TTACTAACAT	TTTAAGTCTA	AAGTAAAAGA	TTGCTTCTGT	ATGTTCTCCC	CCAGGTGTGT	1560
AGGTCCATCC	TGGGAAGGCC	ATCAGACACA	CCTAGTCCAT	GGGTGACACC	CAGCCAGTTT	1620
TTAATGCCAG	TTCCTCTGGC	AGTTTTTAAT	TTAGGCACTC	GGAAGTGAAA	CCCGGACATT	1680
CACTGGAAAT	GACTTTAGGA	CAAGACCTGC	TGGCCATGAG	CTGAGAAATG	TCTTACTCTC	1740
TTGCAGGGAG	AATGCTGTTG	AAAGACTTGA	TTCATTAATA	CAAGCGACTC	ACGTTGCAAT	1800
GAGAGGCAAC	TCCGATTACG	CTGATCTTAG	TGATGGCTGG	CTCGAAATAA	TACGTGTAGA	1860
TGCCCCTGAT	CCAGGTGCAG	ACCCGCTGGC	TAGCAGTGTG	AACGGCATGT	GCCTGGATAT	1920
TCCTGCTCAC	CTGAGCATCC	GCATCCTCAT	CTCGGATGCT	GGCGCGGTGG	AAGGGATTAC	1980
TCAGCAGGAG	ATACTCGGTG	TAGAGACAAG	GTTCTCCTCA	GTGAACTGGC	AGTACCAGTG	2040
TGGGCTTACC	TGTGAGCACA	AGGCCGACCT	TCTCCCTATC	AGTGCATCCG	TCCAGTTTAT	2100
TAAAATTCCT	GCACAGTTAC	CCCACCCCT	GACAAGATTC	CAGATCAATT	ATACAGAGTA	2160
TGACTGCAAC	AGAAATGAGG	TGTGTTGGCC	GCAGCTTCTA	TATCCATGGA	CTCAGTATTA	2220
TCAAGGGGAG	CTGCATTCTC	AGTGTGTTGC	TAAGGGCTTA	CTGTTGCTGT	TGTTCCCTCAC	2280
ATTGGCCTTG	TTCCTCAGCA	ACCCCTGGAC	CAGAATATGC	AAAGCCTATA	GTTAGACAAC	2340

CACCTGGCTT TTATTTTTTT GAGATGGAGT TTTGCTCTTG TTACCCAGGC TGGAGTGCAG 2400  
TGCACAATCT CGGCTCACTG CAATCTCTGC CTCCCAAGCA ATCCTCCCAC CTCAGCCTCT 2460  
GGTGTAGCTG GGACCACAGA TGCTCCACCA TGCCTGGCTG TATTTTTGGT AAAGATGGGG 2520  
TTTCGCCTTG TTGCCCAGGG TGGTCTGTAA CTCCTGAGCT CAGATGATCT GCCCACCTCG 2580  
GCCTCCCAAA GTGCTGGGAT CACAGACGTG AGCCACTGCG TCCGGTCCAT CTGACTTCTC 2640  
AAAGACTTTA GACCTTGACT TCAGTGATTT GTTGTAGTCT TGTATGCTTC TCTATAAAAT 2700  
TTTAATAAAT GAAATGTCTT ATTTTGTAG AAAATTTTAA AAAAAAAAAA AAAA 2754

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Met Arg Gly Asn Ser Asp Tyr Ala Asp Leu Ser Asp Gly Trp Leu Glu  
1 5 10 15  
Ile Ile Arg Val Asp Ala Pro Asp Pro Gly Ala Asp Pro Leu Ala Ser  
20 25 30  
Ser Val Asn Gly Met Cys Leu Asp Ile Pro Ala His Leu Ser Ile Arg  
35 40 45  
Ile Leu Ile Ser Asp Ala Gly Ala Val Glu Gly Ile Thr Gln Gln Glu  
50 55 60  
Ile Leu Gly Val Glu Thr Arg Phe Ser Ser Val Asn Trp Gln Tyr Gln  
65 70 75 80  
Cys Gly Leu Thr Cys Glu His Lys Ala Asp Leu Leu Pro Ile Ser Ala  
85 90 95  
Ser Val Gln Phe Ile Lys Ile Pro Ala Gln Leu Pro His Pro Leu Thr  
100 105 110  
Arg Phe Gln Ile Asn Tyr Thr Glu Tyr Asp Cys Asn Arg Asn Glu Val  
115 120 125  
Cys Trp Pro Gln Leu Leu Tyr Pro Trp Thr Gln Tyr Tyr Gln Gly Glu  
130 135 140  
Leu His Ser Gln Cys Val Ala Lys Gly Leu Leu Leu Leu Phe Leu

145                                      150                                      155                                      160

Thr Leu Ala Leu Phe Leu Ser Asn Pro Trp Thr Arg Ile Cys Lys Ala

   165                                      170                                      175

Tyr Ser

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1363 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

TAGGCCATGA AGGCCGGTTT TTCATAAAAT AGGAATGAGG ACAAATGTTG CTCTTCATCC	60
TACCAGCTGT TTGTTCTTTG GTAGGGGATC ATGAGTGGAA AAACAAAGGC AAGAAGGGCT	120
GCCATGTTTT TTAGACGTTG CTCTGAAGAC GCCAGCGGTA GCGCCAGTGG CAATGCTTTG	180
TTATCAGAGG ACGAAAATCC TGATGCGAAT GGGGTAAGTC GATCATGGAA GATTATTCTA	240
AGTACAATGC TTAACTGAC TTTTCTTCTT GTAGGACTCC TAAATCATCA GTGGCTTAAA	300
GAAACAGATG TTCCTCAGAA ATCCAGACAA TTATATGCCA TAATTGCAGA ATATGGTTCA	360
AGGCTTTATA AATATCAGGC CAGACTTCGT ATGCCTAAAG AGCAACTGGA ACTTTTAAAG	420
AAGGAAAGCC AGAATCTGGA AAACAATTTT CGTCAAATTC TATTTTGTAT CGAACAAATA	480
GATGTCCTGA AGGCATTGCT AAGAGATATG AAGGATGGTA TGGACAATAA TCACAAGTGG	540
AACACCCATG GAGACCTGT GGAGGACCCG GACCACACAG AGGAAGTGTC AAAGTTGGTC	600
AATTATGTAC TTAAAAAGTT GAGAGAAGAC CAAGTCGAGA TGGCTGATTA TGCCCTGAAG	660
TCGGCCGGAG CCTCCATCAT TGAAGCTGGG ACCTCAGAAA GTTATAAAAA TAATAAAGCA	720
AAATTGTACT GGCATGGGAT AGGTTTCCTA AATCATGAAA TGCCTCCAGA TATTATTCTT	780
CAGCCGGATG TCTACCCTGG AAAGTGCTGG GCTTTTCCAG GTTCCCAGGG TCATACCCTA	840
ATCAAGCTTT ACAAAGATCA TACCAACTGC TGTTACCATG GAGCACATCT CAGAGAAGGT	900
GTCTCCGTCA GGAAACATCT CCAGTGCACC CAAGGAATTT TCTGTCTATG GCATCACAAA	960
AAAATGTGAA GGAGAAGAAA TTTTCCTAGG TCAGTTTATA TATAACAAA CAGGAACCAC	1020
CGTTCAAACA TTTGAACTCC AGCATGCAGT TTCTGAATAT TTATTATGTG TGAAACTTAA	1080

TATCTTTAGC AACTGGGGAC ACCCGAAGTA TACTTGTTTA TATCGATTCA GGGTCCATGG 1140  
CACACCAGGC AAGCACATCT AGAAGAGTTG GTACAGAAGG CCATGCCACA TGTCCAGAAT 1200  
ATTCAAGAAT GCTTATTCTC TTAGATGATA CCGCACCCAT AGGAATTGAG AATTGGGAGT 1260  
GGGAAGAAAA CCTCAAAGTG GTTCATACTT GCCTGTAAAA AGTAAATGCA TTTTACTAAT 1320  
AAAAAATAT GGAAGTAAAT TAAAAA AAA 1363

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Met	Ser	Gly	Lys	Thr	Lys	Ala	Arg	Arg	Ala	Ala	Met	Phe	Phe	Arg	Arg	1	5	10	15
Cys	Ser	Glu	Asp	Ala	Ser	Gly	Ser	Ala	Ser	Gly	Asn	Ala	Leu	Leu	Ser	20	25	30	
Glu	Asp	Glu	Asn	Pro	Asp	Ala	Asn	Gly	Val	Thr	Arg	Ser	Trp	Lys	Ile	35	40	45	
Ile	Leu	Ser	Thr	Met	Leu	Thr	Leu	Thr	Phe	Leu	Leu	Val	Gly	Leu	Leu	50	55	60	
Asn	His	Gln	Trp	Leu	Lys	Glu	Thr	Asp	Val	Pro	Gln	Lys	Ser	Arg	Gln	65	70	75	80
Leu	Tyr	Ala	Ile	Ile	Ala	Glu	Tyr	Gly	Ser	Arg	Leu	Tyr	Lys	Tyr	Gln	85	90	95	
Ala	Arg	Leu	Arg	Met	Pro	Lys	Glu	Gln	Leu	Glu	Leu	Leu	Lys	Lys	Glu	100	105	110	
Ser	Gln	Asn	Leu	Glu	Asn	Asn	Phe	Arg	Gln	Ile	Leu	Phe	Leu	Ile	Glu	115	120	125	
Gln	Ile	Asp	Val	Leu	Lys	Ala	Leu	Leu	Arg	Asp	Met	Lys	Asp	Gly	Met	130	135	140	
Asp	Asn	Asn	His	Asn	Trp	Asn	Thr	His	Gly	Asp	Pro	Val	Glu	Asp	Pro	145	150	155	160
Asp	His	Thr	Glu	Glu	Val	Ser	Asn	Leu	Val	Asn	Tyr	Val	Leu	Lys	Lys				

165	170	175
Leu Arg Glu Asp Gln Val Glu Met Ala Asp Tyr Ala Leu Lys Ser Ala		
180	185	190
Gly Ala Ser Ile Ile Glu Ala Gly Thr Ser Glu Ser Tyr Lys Asn Asn		
195	200	205
Lys Ala Lys Leu Tyr Trp His Gly Ile Gly Phe Leu Asn His Glu Met		
210	215	220
Pro Pro Asp Ile Ile Leu Gln Pro Asp Val Tyr Pro Gly Lys Cys Trp		
225	230	235
Ala Phe Pro Gly Ser Gln Gly His Thr Leu Ile Lys Leu Tyr Lys Asp		
245	250	255
His Thr Asn Cys Cys Tyr His Gly Ala His Leu Arg Glu Gly Val Ser		
260	265	270
Val Arg Lys His Leu Gln Cys Thr Gln Gly Ile Phe Cys Leu Trp His		
275	280	285
His Lys Lys Met		
290		

(2) INFORMATION FOR SEQ ID NO:137:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2911 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

GGGCTGCATT TCCAGCAGGA GCTGCGAGCA CAGTGCTGGC TCACAACAAG ATGCTCAAGG	60
TGTCAGCCGT ACTGTGTGTG TGTGCAGCCG CTTGGTGCAG TCAGTCTCTC GCAGCTGCCG	120
CGGCGGTGGC TGCAGCCGGG GGGCGGTCGG ACGGCGGTAA TTTTCTGGAT GATAACAAT	180
GGCTCACCAC AATCTCTCAG TATGACAAGG AAGTCGGACA GTGGAACAAA TTCCGAGACG	240
AAGTAGAGGA TGATTATTTT CGCACTTGGA GTCCAGGAAA ACCCTTCGAT CAGGCTTTAG	300
ATCCAGCTAA GGATCCATGC TTAAAGATGA AATGTAGTCG CCATAAAGTA TGCATTGCTC	360
AAGATTCTCA GACTGCAGTC TGCATTAGTC ACCGGAGGCT TACACACAGG ATGAAAGAAG	420
CAGGAGTAGA CCATAGGCAG TGGAGGGGTC CCATATTATC CACCTGCAAG CAGTGCCAG	480
TGGTCTATCC CAGCCCTGTT TGTGGTTCAG ATGGTCATAC CTACTCTTTT CAGTGCAAAC	540

TAGAATATCA	GGCATGTGTC	TTAGGAAAAC	AGATCTCAGT	CAAATGTGAA	GGACATTGCC	600
CATGTCCTTC	AGATAAGCCC	ACCAGTACAA	GCAGAAATGT	TAAGAGAGCA	TGCAGTGACC	660
TGGAGTTCAG	GGAAGTGGCA	AACAGATTGC	GGGACTGGTT	CAAGGCCCTT	CATGAAAGTG	720
GAAGTCAAAA	CAAGAAGACA	AAAACATTGC	TGAGGCCTGA	GAGAAGCAGA	TTCGATACCA	780
GCATCTTGCC	AATTTGCAAG	GACTCACTTG	GCTGGATGTT	TAACAGACTT	GATACAAACT	840
ATGACCTGCT	ATTGGACCAG	TCAGAGCTCA	GAAGCATTTA	CCTTGATAAG	AATGAACAGT	900
GTACCAAGGC	ATTCTTCAAT	TCTTGTGACA	CATACAAGGA	CAGTTTAATA	TCTAATAATG	960
AGTGGTGCTA	CTGCTTCCAG	AGACAGCAAG	ACCCACCTTG	CCAGACTGAG	CTCAGCAATA	1020
TTCAGAAGCG	GCAAGGGGTT	AAGAAGCTCC	TAGGACAGTA	TATCCCCCTG	TGTGATGAAG	1080
ATGGTTACTA	CAAGCCAACA	CAATGTCATG	GCAGTGTTGG	ACAGTGCTGG	TGTGTTGACA	1140
GATATGGAAA	TGAAGTCATG	GGATCCAGAA	TAAATGGTGT	TGCAGATTGT	GCTATAGATT	1200
TTGAGATCTC	CGGAGATTTT	GCTAGTGGCG	ATTTTCATGA	ATGGACTGAT	GATGAGGATG	1260
ATGAAGACGA	TATTATGAAT	GATGAAGATG	AAATTGAAGA	TGATGATGAA	GATGAAGGGG	1320
ATGATGATGA	TGGTGGTGAT	GACCATGATG	TATACATTTA	ATTGATGACA	GTTGAAATCA	1380
ATAAATTCTA	CATTTCTAAT	ATTTACAAAA	ATGATAGCCT	ATTTAAAATT	ATCTTCTTCC	1440
CCAATAACAA	AATGATTCTA	AACCTCACAT	ATATTTTGTA	TAATTATTTG	AAAAATTGCA	1500
GCTAAAGTTA	TAGAACTTTA	TGTTTAAATA	AGAATCATTT	GCTTTGAGTT	TTTATATTCC	1560
TTACACAAAA	AGAAAATACA	TATGCAGTCT	AGTCAGACAA	AATAAAGTTT	TGAAGTGCTA	1620
CTATAATAAG	TTTTTCACGA	GAACAACTT	TGTAAATCTT	CCATAAGCAA	AATGACAGCT	1680
AGTGCTTGGG	ATCGTACATG	TTAATTTTCT	GAAAGATAAT	TCTAAGTGAA	ATTTAAAATA	1740
AATAAATTTT	TAATGACCTG	GGTCTTAAGG	ATTTAGGAAA	AATATGCATG	CTTTAATTGC	1800
ATTTCCAAAG	TAGCATCTTG	CTAGACCTAG	TTGAGTCAGG	ATAACAGAGA	GATACCACAT	1860
GGCAAGAAAA	ACAAAGTGAC	AATTGTAGAG	TCCTCAATTG	TGTTTACATT	AATAGTGGTG	1920
TTTTTACCTA	TGAAATTATT	CTGGATCTAA	TAGGACATTT	TACAAAATGG	CAAGTATGGA	1980
AAACCATGGA	TTCTGAAAGT	TAAAAATTTA	GTTGTTCTCC	CCAATGTGTA	TTTAAATTTG	2040
GATGGCAGTC	TCATGCAGAT	TTTTTAAAAG	ATTCTTTAAT	AACATGATTT	GTTTGCCTTT	2100
CTAGATTTCT	TTATCTTTCT	GACCAGCAAC	TTAGGGAGCA	GAATTTAAAT	TAGGAAGACA	2160
AAGGGAAAGA	TTCATTTAAA	CCATATTTTT	ACAAAGTTTG	TCATTTGCCC	CAAGGTCAAA	2220

TTTTAAATTC TTAATTTTCA TTTTATTTCC CATTTTAGGT AAAAGTTTGC ATTTAATCTT 2280  
 AGAATTATGT TATTTTGTGTT AGTAGTGTGG AAACCTTAGAG AACCTTATTGT ATGGTGCCTT 2340  
 GCAAAAATAG AGATAGAAAG ATTTTAGCAT GCATACCAAT ATAGTATATT ACGCAATATA 2400  
 TAAGCACACC TAATTAACAG ATTAATATCA GTAAAGGTAT TGCTGCTGGA ATGAAGAAAA 2460  
 TGGGATACGT TTGTTTCTTT TTTTCTATTG TWACATAATT GCCATGTGGA CTTGTTTATG 2520  
 ATTATTGTGT AGAGTAGCAT TTAAGATTTA ACTGTAGCAA AAATTACTTT AACCGCTGTA 2580  
 TTTAAGTTAG CATGTTAATT AATTGTGTAG ACATTTTGGC ACACCATCAC TTTTAACTAT 2640  
 ATCATACCAA TGGTTTGTG CCCATAATAA AAATGGAAAA ACCTGTTGAA TGTTACGTAT 2700  
 TGGTATCTTT AATTCAACA GTGGGTAAAC TGGTTTCCCA GTATACAATT CATTGAAAGC 2760  
 AAAATTGATT AATTATTTCC ATTTAATTTA TACACACTCA ATACAAAATT TAATGTTGAC 2820  
 TTTACGTAAT AAAGTATAAT GCATTTTCTT TTTTACTGTT TATGTATAGT TTACAAAATA 2880  
 AAGAATCTTG TAACCAAAAA AAAAAAAAAA A 2911

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 436 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

Met	Leu	Lys	Val	Ser	Ala	Val	Leu	Cys	Val	Cys	Ala	Ala	Ala	Trp	Cys
1															15
Ser	Gln	Ser	Leu	Ala	Ala	Ala	Ala	Ala	Val	Ala	Ala	Ala	Gly	Gly	Arg
			20						25					30	
Ser	Asp	Gly	Gly	Asn	Phe	Leu	Asp	Asp	Lys	Gln	Trp	Leu	Thr	Thr	Ile
		35					40						45		
Ser	Gln	Tyr	Asp	Lys	Glu	Val	Gly	Gln	Trp	Asn	Lys	Phe	Arg	Asp	Glu
		50				55					60				
Val	Glu	Asp	Asp	Tyr	Phe	Arg	Thr	Trp	Ser	Pro	Gly	Lys	Pro	Phe	Asp
65					70					75				80	
Gln	Ala	Leu	Asp	Pro	Ala	Lys	Asp	Pro	Cys	Leu	Lys	Met	Lys	Cys	Ser
				85					90					95	



Arg His Lys Val Cys Ile Ala Gln Asp Ser Gln Thr Ala Val Cys Ile  
 100 105 110  
 Ser His Arg Arg Leu Thr His Arg Met Lys Glu Ala Gly Val Asp His  
 115 120 125  
 Arg Gln Trp Arg Gly Pro Ile Leu Ser Thr Cys Lys Gln Cys Pro Val  
 130 135 140  
 Val Tyr Pro Ser Pro Val Cys Gly Ser Asp Gly His Thr Tyr Ser Phe  
 145 150 155 160  
 Gln Cys Lys Leu Glu Tyr Gln Ala Cys Val Leu Gly Lys Gln Ile Ser  
 165 170 175  
 Val Lys Cys Glu Gly His Cys Pro Cys Pro Ser Asp Lys Pro Thr Ser  
 180 185 190  
 Thr Ser Arg Asn Val Lys Arg Ala Cys Ser Asp Leu Glu Phe Arg Glu  
 195 200 205  
 Val Ala Asn Arg Leu Arg Asp Trp Phe Lys Ala Leu His Glu Ser Gly  
 210 215 220  
 Ser Gln Asn Lys Lys Thr Lys Thr Leu Leu Arg Pro Glu Arg Ser Arg  
 225 230 235 240  
 Phe Asp Thr Ser Ile Leu Pro Ile Cys Lys Asp Ser Leu Gly Trp Met  
 245 250 255  
 Phe Asn Arg Leu Asp Thr Asn Tyr Asp Leu Leu Leu Asp Gln Ser Glu  
 260 265 270  
 Leu Arg Ser Ile Tyr Leu Asp Lys Asn Glu Gln Cys Thr Lys Ala Phe  
 275 280 285  
 Phe Asn Ser Cys Asp Thr Tyr Lys Asp Ser Leu Ile Ser Asn Asn Glu  
 290 295 300  
 Trp Cys Tyr Cys Phe Gln Arg Gln Gln Asp Pro Pro Cys Gln Thr Glu  
 305 310 315 320  
 Leu Ser Asn Ile Gln Lys Arg Gln Gly Val Lys Lys Leu Leu Gly Gln  
 325 330 335  
 Tyr Ile Pro Leu Cys Asp Glu Asp Gly Tyr Tyr Lys Pro Thr Gln Cys  
 340 345 350  
 His Gly Ser Val Gly Gln Cys Trp Cys Val Asp Arg Tyr Gly Asn Glu  
 355 360 365  
 Val Met Gly Ser Arg Ile Asn Gly Val Ala Asp Cys Ala Ile Asp Phe  
 370 375 380  
 Glu Ile Ser Gly Asp Phe Ala Ser Gly Asp Phe His Glu Trp Thr Asp  
 385 390 395 400

Asp Glu Asp Asp Glu Asp Asp Ile Met Asn Asp Glu Asp Glu Ile Glu  
405 410 415

Asp Asp Asp Glu Asp Glu Gly Asp Asp Asp Asp Gly Gly Asp Asp His  
420 425 430

Asp Val Tyr Ile  
435

(2) INFORMATION FOR SEQ ID NO:139:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 4130 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

GGATTCTGAAG TTTAAGAAAC TGCATTTTAA AGTGCCCAAA GTTTCATTTT CTTCTACCAA	60
AACTCCTAAA GATAGTTTAG TCCCAGGTGC AAAGTCTAGC ATAGGTCTTT CCACGATTCC	120
TTTATCATCT TCAGAATGCT CAAGTTTTGA ATTACAACAG GTTTCGGCTT GTTCAGAGCC	180
ATCCATGCAG ATGCCTAAGG TGGGTTTTGC TGGGTTTCCA TCATCCCGGC TTGATCTCAC	240
TGGTCCCTCAC TTTGAATCTT CTATTCTCTC TCCCTGTGAG GATGTTACAC TTACAAAATA	300
CCAGGTGACT GTTCCCCAGA GCTGCCTTGG CCCCTGAGCT TGCTCTGGAA ATTCCTTCTG	360
GGTCTCAGGC TGATATTCCT CTTCCAAGA CAGAGTGCTC CACTGAMCTG CAGCCTCCAG	420
ARGGAGTTCC AACATCTCAA GCTGAGAGTC ACTCTGGCCC ACTGAATTCC ATGATTCCTG	480
TTTCTCTTGG TCAGGTGTCT TTTCTAAAT TCTATAAACC AAAGTTTGTG TTTTCAGTCC	540
CCCAAATGGC AGTTCCTGAG GGAGACCTAC ATGCAGCAGT GGGTGCCCCA GTCATGTYTC	600
YTCTTAGCCC TTGGAGAAAG AGTGCAGTGC CCCTTGCCAA GCACCCAGYT GCCATCCCCA	660
GGCACCTGTG TGTCCCAGGG CCCAGAAGAG CTTGTGGCCT CTTGCAGAC ATCAGTAGTG	720
GCCCYTGAG AAGCCCCTTC TGAAGATGCT GACCACGAAG GGAAAGGGAG TCCCTTGAAA	780
ATGCCTAAGA TTAAGCTTCC ATCATTTAGG TGGTCCCCGA AGAAGGAAAC AGGGCCAAAG	840
GTGGACCCAG AATGCAGCGT GGAGGACTCA AAATCAGCC TGGTTTTAGA CAAGGATGAA	900
GTGGCCCCGC AGTCTGCCAT CCACATGGAT CTGCCTCCTG AGAGGGATGG AGAGAAGGGG	960
AGGAGCACAA AGCCTGGCTT TGCCATGCCA AAATCTGCAC TTCCCAAAT GAAGGCTTCT	1020

AAGAGTGGGG	TCAGCCTGCC	ACAGAGAGAC	GTGGATCCTT	CCCTTTCTAG	TGCCACAGCA	1080
GGGGGTAGCT	TTCAAGACAC	AGAAAAGGCC	AGCAGTGACG	GTGGTAGGGG	AGGACTTGGT	1140
GCAACAGCAA	GTGCCACAGG	AAGTGAGGGT	GTGAACCTCC	ACCGGCCACA	GGTCCACATT	1200
CCCAGTTTGG	GCTTTGCCAA	ACCTGATCTC	AGATCCTCCA	AGGCCAAGGT	GGAGGTGAGC	1260
CAGCCTGAAG	CTGACCTGCC	TCTTCCCAAA	CATGATCTGT	CTACCGAAGG	TGACAGCAGA	1320
GGATGTGGGC	TCGAGGATGT	CCCAGTGAGC	CAGCCTTGTG	GGGAGGGGAT	AGCCCCCACA	1380
CCTGAAGATC	CCCTCCAGCC	ATCCTGTAGA	AAACCAGATG	CTGAAGTCCT	CACAGTGGAA	1440
AGCCCAGAGG	AGGAAGCCAT	GACCAAGGAC	TCGCAGGAAA	GCTGGTTTAA	AATGCCCAAG	1500
TTCCGCATGC	CCAGCCTTAG	GCGCTCTTTC	AGGGACAGAG	GCGGGGCTGG	AAAGCTGGAA	1560
GTGGCTCAGA	CACAGGCACC	GGCAGCAACA	GGGGGTGAAG	CAGCAGCTAA	AGTCAAAGAG	1620
TTCTTGTTTT	CTGGGTCAAA	CGTGGAGGCA	GCTATGTCCC	TACAGCTCCC	AGAGGCAGAT	1680
GCAGAAGTGA	CAGCTTCTGA	GAGCAAATCA	TCCACAGATA	TTCTAAGGTG	TGATCTTGAC	1740
AGCACAGGCT	TGAAGCTGCA	CCTTTCCACT	GCTGGGATGA	CTGGGGATGA	GCTTTCCACT	1800
TCTGAGGTCA	GGATCCATCC	ATCCAAAGGA	CCTCTCCCTT	TTCAGATGCC	TGGCATGAGG	1860
CTTCCAGAAA	CCCAGGTTCT	TCCAGGAGAA	ATAGATGAGA	CTCCTCTTTC	CAAGCCAGGA	1920
CATGACCTTG	CCAGCATGGA	GGATAAAACA	GAGAAATGGT	CTTCCCAGCC	TGAAGGTCCA	1980
CTTAAATTGA	AAGCTTCAAG	TACTGATATG	CCATCCCAGA	TTTCTGTGGT	TAATGTGGAT	2040
CAACTGTGGG	AAGATTCTGT	CCTAACTGTC	AAATTCCCCA	AATTAATGGT	ACCAAGGTTC	2100
TCCTTCGCTG	CCCCCAGCTC	AGAGGATGAT	GTGTTTCATCC	CCACTGTGAG	GGAAGTGCAG	2160
TGTCCAGAGG	CCAATATTGA	TACAGCCCTT	TGTAAGGAAA	GTCCGGGGCT	CTGGGGAGCC	2220
AGCATCCTGA	AGGCAGGTGC	TGGGGTCCCT	GGGGAGCAGC	CTGTGGACCT	TAACCTGCCT	2280
TTGGAAGCTC	CCCCAATTTC	AAAGGTCAGA	GTGCATATTC	AGGGTGCTCA	GGTTGAAAGT	2340
CAAGAGGTCA	CTATACACAG	CATAGTGACA	CCAGAGTTTG	TAGATCTCTC	AGTACCCAGG	2400
ACTTTTTCCA	CTCAGATTGT	GCGGGAATCA	GAGATCCCCA	CGTCAGAGAT	TCAAACACCT	2460
TCGTACGGAT	TTTCCTTATT	AAAAGTGAAA	ATCCCAGAGC	CCCACACGCA	GGCTAGAGTG	2520
TACACAACAA	TGACTCAACA	CTCTAGGACT	CAGGAGGGCA	CAGAAGAGGC	TCCCATACAA	2580
GCCACCCCAG	GAGTAGACTC	CATTTCTGGA	GATCTCCAGC	CTGACACTGG	AGAACCATTT	2640
GAGATGATCT	CTTCCAGCGT	CAATGTACTG	GGACAGCAAA	CACTCACATT	TGAAGTTCCT	2700

TCTGGCCACC AGCTTGCAGA CAGCTGTTCA GATGAGGAGC CAGCAGAAAT TCTTGAGTTT	2760
CCCCCTGATG ATAGCCAAGA GGCAACCACA CCACTGGCAG ATGAAGGCAG GGCTCCAAAA	2820
GACAAACCAG AAAGTAAAAA ATCTGGTCTG CTCTGGTTTT GGCTTCCAAA CATTGGGTTT	2880
TCCTCTTCTG TTGATGAGAC AGGTGTTGAT TCCAAAAATG ACGTCCAGAG ATCTGCTCCC	2940
ATTCAAACAC AGCCTGAGGC ACGACCAGAG GCAGAAGTGC CTAAAAACA GGAGAAGGCA	3000
GGCTGGTTCC GATTTCCCAA ATTAGGGTTC TCCTCATCTC CTACCAAGAA AAGCAAAAGC	3060
ACCGAAGATG GGGCAGAGCT GGAAGAACAA AAAC TTCAAG AAGAAACAAT CACGTTTTTC	3120
GATGCCCCGAG AAAGTTTCTC CCCTGAAGAG AAGGAAGAGG GTGAACTGAT CGGGCCTGTG	3180
GGCACTGGGC TGGACTCCAG AGTGATGGTG ACATCCGCGG CAAGAACAGA GTTAATCCTG	3240
CCCGAGCAGG ACAGAAAAGC TGACGATGAA AGCAAAGGGT CAGGCCTGGG ACCAAATGAA	3300
GGCTGAGAGG TATGGCTCAT CGGTACAAGA GAGATGCAAA AAAC TAAGTT GGAAAGTAAA	3360
GGCTACACAC ACATATGGAG CACCCCATCC CACAGCACAT TACATCCACC TCACTTCACA	3420
GAACGGAGAA CAGAGCAGAA ATGACCAGAA CACCTTTGTC ACCATCACAC AGCCCTCCTA	3480
AAATGGAACC AAAGCTTCCC AGCTCCCTCA AAGCTTTGGA TGCAAAGAAG GCACCCTGAC	3540
TTCCACAAGA CACCAGAATT CACACGGTAC TCAGAGGCAC TGCTGGGGAA GTTTGTTGGT	3600
CTTTATTAGA TAAATT TCCA GAGACCTGTC CATAATACCC AACAGAACAT GACTGTTTCT	3660
TTGAGGAAAG GGT TATAATG TCTGTGGTGT ACAAGTCGTT TTTGGTATAA CTTCTTTCCT	3720
GCTGCTGCTG CTTCCCGGCA AACATAGTTT TCCTATTTCA GGCAGAGTGC GGTATATTCC	3780
AGGAAACACT GTTTCCTACT CACTTAGCTT ACTTCTTTGT TGAATGCCTC ACTAATGGCA	3840
AGTTTCAAGA TGTTTTGGGT GACAATGCAC ACATGCTGGG CAAAAGGGTG ATGGCCAGTG	3900
GCTGGCAGCT GGGCCAGCAG AAGCTAGGAC ATCTGTGAGT TGTCATTCTC ATCTATCCAT	3960
GTCCACTGGC CTGCCAGCAT CCGCCAGTGC CTTGCCAGTG TGCACGGTCC CACACTGTGG	4020
CCCCTGAGTC CCCTAATGTA CACGCTGCAG CCAGAATGCA GATGGAGCTG GCTTGGCTGT	4080
TCCCTGGATG GGCAATAAAG AAAGTGCTGC ATCCCAAAAA AAAAAAAAAA	4130

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 911 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

Met	Gln	Gln	Trp	Val	Pro	Gln	Ser	Cys	Xaa	Xaa	Leu	Ala	Leu	Gly	Glu	
1				5					10					15		
Arg	Val	Gln	Cys	Pro	Leu	Pro	Ser	Thr	Gln	Leu	Pro	Ser	Pro	Gly	Thr	
			20					25					30			
Cys	Val	Ser	Gln	Gly	Pro	Glu	Glu	Leu	Val	Ala	Ser	Leu	Gln	Thr	Ser	
			35				40					45				
Val	Val	Ala	Xaa	Gly	Glu	Ala	Pro	Ser	Glu	Asp	Ala	Asp	His	Glu	Gly	
	50					55					60					
Lys	Gly	Ser	Pro	Leu	Lys	Met	Pro	Lys	Ile	Lys	Leu	Pro	Ser	Phe	Arg	
65				70						75					80	
Trp	Ser	Pro	Lys	Lys	Glu	Thr	Gly	Pro	Lys	Val	Asp	Pro	Glu	Cys	Ser	
				85					90					95		
Val	Glu	Asp	Ser	Lys	Leu	Ser	Leu	Val	Leu	Asp	Lys	Asp	Glu	Val	Ala	
			100					105					110			
Pro	Gln	Ser	Ala	Ile	His	Met	Asp	Leu	Pro	Pro	Glu	Arg	Asp	Gly	Glu	
			115				120					125				
Lys	Gly	Arg	Ser	Thr	Lys	Pro	Gly	Phe	Ala	Met	Pro	Lys	Leu	Ala	Leu	
	130					135					140					
Pro	Lys	Met	Lys	Ala	Ser	Lys	Ser	Gly	Val	Ser	Leu	Pro	Gln	Arg	Asp	
145					150					155					160	
Val	Asp	Pro	Ser	Leu	Ser	Ser	Ala	Thr	Ala	Gly	Gly	Ser	Phe	Gln	Asp	
				165					170					175		
Thr	Glu	Lys	Ala	Ser	Ser	Asp	Gly	Gly	Arg	Gly	Gly	Leu	Gly	Ala	Thr	
			180					185					190			
Ala	Ser	Ala	Thr	Gly	Ser	Glu	Gly	Val	Asn	Leu	His	Arg	Pro	Gln	Val	
			195				200					205				
His	Ile	Pro	Ser	Leu	Gly	Phe	Ala	Lys	Pro	Asp	Leu	Arg	Ser	Ser	Lys	
	210					215					220					
Ala	Lys	Val	Glu	Val	Ser	Gln	Pro	Glu	Ala	Asp	Leu	Pro	Leu	Pro	Lys	
225					230					235					240	
His	Asp	Leu	Ser	Thr	Glu	Gly	Asp	Ser	Arg	Gly	Cys	Gly	Leu	Glu	Asp	
				245					250					255		
Val	Pro	Val	Ser	Gln	Pro	Cys	Gly	Glu	Gly	Ile	Ala	Pro	Thr	Pro	Glu	
				260				265						270		

Asp Pro Leu Gln Pro Ser Cys Arg Lys Pro Asp Ala Glu Val Leu Thr  
 275 280 285  
 Val Glu Ser Pro Glu Glu Glu Ala Met Thr Lys Asp Ser Gln Glu Ser  
 290 295 300  
 Trp Phe Lys Met Pro Lys Phe Arg Met Pro Ser Leu Arg Arg Ser Phe  
 305 310 315 320  
 Arg Asp Arg Gly Gly Ala Gly Lys Leu Glu Val Ala Gln Thr Gln Ala  
 325 330 335  
 Pro Ala Ala Thr Gly Gly Glu Ala Ala Ala Lys Val Lys Glu Phe Leu  
 340 345 350  
 Val Ser Gly Ser Asn Val Glu Ala Ala Met Ser Leu Gln Leu Pro Glu  
 355 360 365  
 Ala Asp Ala Glu Val Thr Ala Ser Glu Ser Lys Ser Ser Thr Asp Ile  
 370 375 380  
 Leu Arg Cys Asp Leu Asp Ser Thr Gly Leu Lys Leu His Leu Ser Thr  
 385 390 395 400  
 Ala Gly Met Thr Gly Asp Glu Leu Ser Thr Ser Glu Val Arg Ile His  
 405 410 415  
 Pro Ser Lys Gly Pro Leu Pro Phe Gln Met Pro Gly Met Arg Leu Pro  
 420 425 430  
 Glu Thr Gln Val Leu Pro Gly Glu Ile Asp Glu Thr Pro Leu Ser Lys  
 435 440 445  
 Pro Gly His Asp Leu Ala Ser Met Glu Asp Lys Thr Glu Lys Trp Ser  
 450 455 460  
 Ser Gln Pro Glu Gly Pro Leu Lys Leu Lys Ala Ser Ser Thr Asp Met  
 465 470 475 480  
 Pro Ser Gln Ile Ser Val Val Asn Val Asp Gln Leu Trp Glu Asp Ser  
 485 490 495  
 Val Leu Thr Val Lys Phe Pro Lys Leu Met Val Pro Arg Phe Ser Phe  
 500 505 510  
 Ala Ala Pro Ser Ser Glu Asp Asp Val Phe Ile Pro Thr Val Arg Glu  
 515 520 525  
 Val Gln Cys Pro Glu Ala Asn Ile Asp Thr Ala Leu Cys Lys Glu Ser  
 530 535 540  
 Pro Gly Leu Trp Gly Ala Ser Ile Leu Lys Ala Gly Ala Gly Val Pro  
 545 550 555 560  
 Gly Glu Gln Pro Val Asp Leu Asn Leu Pro Leu Glu Ala Pro Pro Ile  
 565 570 575

Ser Lys Val Arg Val His Ile Gln Gly Ala Gln Val Glu Ser Gln Glu  
 580 585 590  
 Val Thr Ile His Ser Ile Val Thr Pro Glu Phe Val Asp Leu Ser Val  
 595 600 605  
 Pro Arg Thr Phe Ser Thr Gln Ile Val Arg Glu Ser Glu Ile Pro Thr  
 610 615 620  
 Ser Glu Ile Gln Thr Pro Ser Tyr Gly Phe Ser Leu Leu Lys Val Lys  
 625 630 635 640  
 Ile Pro Glu Pro His Thr Gln Ala Arg Val Tyr Thr Thr Met Thr Gln  
 645 650 655  
 His Ser Arg Thr Gln Glu Gly Thr Glu Glu Ala Pro Ile Gln Ala Thr  
 660 665 670  
 Pro Gly Val Asp Ser Ile Ser Gly Asp Leu Gln Pro Asp Thr Gly Glu  
 675 680 685  
 Pro Phe Glu Met Ile Ser Ser Ser Val Asn Val Leu Gly Gln Gln Thr  
 690 695 700  
 Leu Thr Phe Glu Val Pro Ser Gly His Gln Leu Ala Asp Ser Cys Ser  
 705 710 715 720  
 Asp Glu Glu Pro Ala Glu Ile Leu Glu Phe Pro Pro Asp Asp Ser Gln  
 725 730 735  
 Glu Ala Thr Thr Pro Leu Ala Asp Glu Gly Arg Ala Pro Lys Asp Lys  
 740 745 750  
 Pro Glu Ser Lys Lys Ser Gly Leu Leu Trp Phe Trp Leu Pro Asn Ile  
 755 760 765  
 Gly Phe Ser Ser Ser Val Asp Glu Thr Gly Val Asp Ser Lys Asn Asp  
 770 775 780  
 Val Gln Arg Ser Ala Pro Ile Gln Thr Gln Pro Glu Ala Arg Pro Glu  
 785 790 795 800  
 Ala Glu Leu Pro Lys Lys Gln Glu Lys Ala Gly Trp Phe Arg Phe Pro  
 805 810 815  
 Lys Leu Gly Phe Ser Ser Ser Pro Thr Lys Lys Ser Lys Ser Thr Glu  
 820 825 830  
 Asp Gly Ala Glu Leu Glu Glu Gln Lys Leu Gln Glu Glu Thr Ile Thr  
 835 840 845  
 Phe Phe Asp Ala Arg Glu Ser Phe Ser Pro Glu Glu Lys Glu Glu Gly  
 850 855 860  
 Glu Leu Ile Gly Pro Val Gly Thr Gly Leu Asp Ser Arg Val Met Val  
 865 870 875 880

Thr Ser Ala Ala Arg Thr Glu Leu Ile Leu Pro Glu Gln Asp Arg Lys  
885 890 895

Ala Asp Asp Glu Ser Lys Gly Ser Gly Leu Gly Pro Asn Glu Gly  
900 905 910

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4142 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

GCTCGTCTCG CCGGGCTGTT CGCGGGCAGG CCCTGCCCTG AAGGGACGAA TCGGCTTGGA	60
GCGCGGGAGG TGGAGTCGGC CCCGGCGGTC GCTCCCTGGA CCCAACCCGA GGCTGACCCA	120
KGCCCCTGCC CATGCGGGGC GCCCCTGGCT CGGAAGAGTC CCCCGGGCCG GGAGCAGCTC	180
CAGGCAGCGG CCCCAGAGGA AGAGGAAGAA GGGACAGTGC TCAGCTTGGG GGACCCGGAC	240
CCTCGCCGCG GCATTTGGAG CCGGGGGCAG TCCCGAACTC TGTGCTTGGC ACCGCCGCTC	300
CGAGTAGGGC AGCGCCTGCC GGGACTCTGA CCCGGACCCC CTGCGCCTCG TAGGCGGCGG	360
CGCCGCCGCG CCACCCTGTT CTTCCGTGTC TCCCTCTGCC TGGCGGCAGT CACGGCCAAG	420
AGAGTATTAT GAGGGAGGCC GAGGACTTCA TGCTCCGGAC AGAGAAACGG CGCTGGGATT	480
AGGGATTGCC ACTTCTGAGA GGATGCTGGG AATCTGCAGG GGGAGACGGA AATTCTTGGC	540
TGCCTCGTTG AGTCTTCTCT GCATCCCAGC CATCACCTGG ATTTACCTGT TTTCTGGGAG	600
CTTCGAAGAT GGAAAGCCCG TGTCTCTGTC ACCGCTGGAG TCCCAGGCAC ACAGCCCCAG	660
GTACACGGCC TCCAGCCAGC GGGAGCGCGA GAGCCTGGAG GTGCGCATGC GCGAGGTGGA	720
GGAGGAGAAC CGCGCCCTCC GCAGGCAGCT CAGCCTGGCC CAGGGCCGAG CCCCATCCCA	780
TCGCCGAGGC AACCCTCCA AGACCTACTC CATGGAGGAG GGCCTGGAG ACAGCGAGAA	840
CCTTCGGGCT GGCATCGTGG CAGGCAACAG CTCCGAGTGT GGGCAGCAGC CGGTCGTGGA	900
GAAATGCGAG ACAATCCACG TTGCTATTGT CTGCGCCGGA TACAATGCCA GCCGGGATGT	960
CGTCACCCTG GTCAAATCCG TCCTGTTCCA TAGACGGAAC CCTCTGCACT TCCACCTTAT	1020
TGCTGACTCC ATTGCGGAGC AGATCCTGGC CACGCTCTTC CAGACCTGGA TGGTGCCCGC	1080



TGTGCGTGTG	GACTTCTACA	ATGCAGACGA	GCTCAAGTCT	GAAGTTTCCT	GGATCCCCAA	1140
TAAACATTAC	TCTGGGATTT	ATGGTCTGAT	GAAGCTTGTC	CTGACCAAGA	CTCTTCCTGC	1200
CAACCTGGAG	AGAGTCATCG	TCCTTGACAC	GGATATCACC	TTTGCCACTG	ACATTGCAGA	1260
GCTGTGGGCT	GTGTTCCACA	AGTTCAAAGG	TCAGCAAGTC	CTGGGCTTGG	TGGAGAACCA	1320
GAGTGACTGG	TACCTTGGA	ACCTGTGGAA	AAATCACCGC	CCATGGCCAG	CCCTTGGAAG	1380
AGGCTACAAC	ACAGGGGTGA	TCCTGTTACT	TCTGGATAAG	CTGCGGAAGA	TGAAATGGGA	1440
GCAGATGTGG	AGGCTGACCG	CAGAGAGGGA	GCTCATGGGC	ATGCTCTCTA	CATCCTTAGC	1500
TGACCAGGAT	ATTTTCAATG	CCGTCATCAA	ACAAAACCCC	TTCCTTGTGT	ACCAGCTCCC	1560
CTGCTTCTGG	AATGTGCAGC	TGTCAGACCA	CACCCGCTCC	GAGCAGTGCT	ACAGAGACGT	1620
GTCTGATCTA	AAGGTCATTC	ACTGGAAGTC	CCCCAAGAAG	CTCCGGGTGA	AGAACAAGCA	1680
TGTGGAGTTT	TTTCGCAACC	TCTACCTGAC	CTTCCTGGAG	TATGACGGCA	ATCTTCTGAG	1740
GCGGGAAGTC	TTTGGCTGCC	CCAGTGAGGC	TGATGTCAAC	AGTGAAAACC	TCCAGAAGCA	1800
GCTGTCTGAG	CTGGACGAGG	ACGACCTGTG	CTATGAGTTC	CGGCGAGAGC	GCTTCACTGT	1860
CCACCGCACC	CACCTGTACT	TCCTGCACTA	CGAGTATGAG	CCTGCAGCAG	ACAGCACGGA	1920
CGTCACCCTG	GTCGCTCAGC	TGTCCATGGA	CAGGCTCCAG	ATGCTGGAGG	CCATCTGCAA	1980
GCACTGGGAG	GGGCCCATCA	GCCTGGCCCT	CTACCTGTCA	GACGCCGAGG	CCCAGCAGTT	2040
CCTCCGCTAC	GCACAGGGCT	CTGAGGTGCT	TATGAGCCGC	CACAACGTGG	GCTACCACAT	2100
CGTGTAACAAG	GAGGGCCAGT	TCTACCCCGT	GAACCTGCTG	CGCAACGTGG	CCATGAAGCA	2160
CATCAGCACT	CCCTACATGT	TCCTGTCTGA	CATTGACTTC	CTGCCCATGT	ATGGGCTCTA	2220
TGAGTACCTC	AGGAAGTCTG	TCATCCAGCT	CGATCTTGCC	AACACCAAGA	AAGCAATGAT	2280
TGTCCCCGCG	TTCGAGACAC	TGCGCTACCG	GCTGTCCTTC	CCCAAGTCAA	AAGCGGAGTT	2340
GCTGTCAATG	CTGGACATGG	GGACCCTCTT	CACATTCAGG	TACCACGTCT	GGACGAAAGG	2400
CCACGCACCC	ACAAACTTCG	CCAAGTGGCG	GACCGCCACC	ACGCCTTACC	GGGTTGAGTG	2460
GGAGGCCGAT	TTTGAGCCGT	ATGTTGTTGT	GAGACGTGAC	TGCCCCGAGT	ACGACCGGAG	2520
GTTTGTAGGC	TTTGGCTGGA	ACAAAGTGGC	TCATATCATG	GAGCTGGATG	TGCAGGAGTA	2580
TGAGTTCATT	GTGCTGCCCA	ACGCCTACAT	GATCCACATG	CCTCATGCCC	CCAGCTTCGA	2640
CATTACCAAG	TTCCGTTCCA	ACAAGCAATA	CCGCATCTGT	CTCAAAACCC	TCAAGGAAGA	2700
GTTTCAGCAG	GACATGTCCC	GCCGCTACGG	CTTTGCTGCC	CTGAAATATC	TCACAGCCGA	2760
GAACAACAGC	TAGCACCAAG	AAGCCCACCA	CTAGGGGGAG	ACATGCTGTA	GGGGAAGTGC	2820

CACTCGCTGT TTGGGGCCCG GCCTTCAAAT TCAAAATTGA GCCATGCTTT TTCGGTTTGT	2880
TTTTATTAT CTCTTTGGCC CAGCCAAGCT GCCCTCACTA CAGAGACCTT GGACAAGGAT	2940
CCAGCCAGTC CCTCTCTGCC CCACAACCCT GCATTCCCAG AGGTTAGCTA TGCAGCCCAC	3000
CTAGATGAGT CTCTTCAAGA ATGGGAAATC AAGGGGTGAC AGGGAGTAAA AGGGTTATCA	3060
TCTTACTGCA AAGCCACAAG ATCAGGGCAG GGCTTTAGGA TGTCTGGAT GCTTTTTAAT	3120
AATTATGCTT CCCATCATAA CTGGGGAGAA AGGGAAGTCA GGGTCTAGG GGTATTTCGT	3180
CCCAGGAAAT AGAAGTGAAA TTGTCTTTAT TAAGTGAAAA CTTTCCCCTT TGCCCTGCAA	3240
TGTAGCTGGG CATTCAAACG GAGGGCAAAC CGATGATCTA AACCAACCAC TTGGAAAAAC	3300
CCAATGGGGA CATTGTAACC AGAGGGTCCT GGAGGTGGGG TTGATGGGTT TCCTTATCCC	3360
CAAAGTCACT CCTGTTTTGT TTTGTTTTTC TTTGGGGGTT TTGTTTATTT TTGGGGCTGG	3420
CAATCCAAAA TAGAAAATCT GATCCTTTGA GGCTCTAAAG GAAAATCAGC TGCCCTTACC	3480
AACCACCCTC TATCAGCAGT GGCCCAGGAA GGAGGTCAAG CATCTTCGGC CGATATTTAA	3540
ACATGGGCAG CTCCTTCAG GATGATCACC GAGGCTCCCG TGACTTTGAA CTCCCTACTC	3600
TCCAGAATCC AGGGGCTATA GCGATGGGGA CTGCGGAATT ACGAGGGCTG GCTGTTTTAC	3660
ACCGGTCACA TTTTCTATTG GCAGTGA CTG ATT CATGGGA AAGGGCTTTG AAGGAACTAC	3720
TTCA GTGCAC ACACAAGGTA CGAACCTYTC AGGCCTTTTCG AAGAACTTTC ATAATTCATG	3780
AAAGCCCAGT TYTGAAGATT CACGTATCCA TYTGAGAGACC TACAGGAAGA AAGTGATTGG	3840
GTCCTCTGG TTCTTGCTG CTC TCACTGTG GATGGGAAGA GGTGACAACC TCAGTCTCCC	3900
TTTGGGACCT GTCCAAGGGT AGGCAACCAC CTTACCTTC ACACAGATTG AGGAGACACT	3960
GGACTTTTTA CCCATTTTCT TTAATYTTCA ATATTAATAT TGTGTTTACA TTGATGAGAA	4020
CAAGAGTTAA TGCCCTACCC TCTGCTGGGC TGTTTGTATT GAGTTGCAAT GTGACCAGCG	4080
AAAGCTGCAT TTAATAAATG AAAGTACAGA CTGAAAAAAAA AAAAAAAAAA AAAAAAAAAA	4140
AA	4142

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 756 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

Met	Leu	Gly	Ile	Cys	Arg	Gly	Arg	Arg	Lys	Phe	Leu	Ala	Ala	Ser	Leu	
1				5					10					15		
Ser	Leu	Leu	Cys	Ile	Pro	Ala	Ile	Thr	Trp	Ile	Tyr	Leu	Phe	Ser	Gly	
			20					25					30			
Ser	Phe	Glu	Asp	Gly	Lys	Pro	Val	Ser	Leu	Ser	Pro	Leu	Glu	Ser	Gln	
		35					40					45				
Ala	His	Ser	Pro	Arg	Tyr	Thr	Ala	Ser	Ser	Gln	Arg	Glu	Arg	Glu	Ser	
	50						55				60					
Leu	Glu	Val	Arg	Met	Arg	Glu	Val	Glu	Glu	Glu	Asn	Arg	Ala	Leu	Arg	
65					70					75					80	
Arg	Gln	Leu	Ser	Leu	Ala	Gln	Gly	Arg	Ala	Pro	Ser	His	Arg	Arg	Gly	
				85					90					95		
Asn	His	Ser	Lys	Thr	Tyr	Ser	Met	Glu	Glu	Gly	Thr	Gly	Asp	Ser	Glu	
			100					105					110			
Asn	Leu	Arg	Ala	Gly	Ile	Val	Ala	Gly	Asn	Ser	Ser	Glu	Cys	Gly	Gln	
		115					120					125				
Gln	Pro	Val	Val	Glu	Lys	Cys	Glu	Thr	Ile	His	Val	Ala	Ile	Val	Cys	
	130					135					140					
Ala	Gly	Tyr	Asn	Ala	Ser	Arg	Asp	Val	Val	Thr	Leu	Val	Lys	Ser	Val	
145				150						155					160	
Leu	Phe	His	Arg	Arg	Asn	Pro	Leu	His	Phe	His	Leu	Ile	Ala	Asp	Ser	
				165					170					175		
Ile	Ala	Glu	Gln	Ile	Leu	Ala	Thr	Leu	Phe	Gln	Thr	Trp	Met	Val	Pro	
		180						185					190			
Ala	Val	Arg	Val	Asp	Phe	Tyr	Asn	Ala	Asp	Glu	Leu	Lys	Ser	Glu	Val	
	195						200					205				
Ser	Trp	Ile	Pro	Asn	Lys	His	Tyr	Ser	Gly	Ile	Tyr	Gly	Leu	Met	Lys	
	210					215					220					
Leu	Val	Leu	Thr	Lys	Thr	Leu	Pro	Ala	Asn	Leu	Glu	Arg	Val	Ile	Val	
225					230					235					240	
Leu	Asp	Thr	Asp	Ile	Thr	Phe	Ala	Thr	Asp	Ile	Ala	Glu	Leu	Trp	Ala	
				245					250					255		
Val	Phe	His	Lys	Phe	Lys	Gly	Gln	Gln	Val	Leu	Gly	Leu	Val	Glu	Asn	
			260				265						270			
Gln	Ser	Asp	Trp	Tyr	Leu	Gly	Asn	Leu	Trp	Lys	Asn	His	Arg	Pro	Trp	

275					280					285				
Pro	Ala	Leu	Gly	Arg	Gly	Tyr	Asn	Thr	Gly	Val	Ile	Leu	Leu	Leu
290					295					300				
Asp	Lys	Leu	Arg	Lys	Met	Lys	Trp	Glu	Gln	Met	Trp	Arg	Leu	Thr
305					310					315				320
Glu	Arg	Glu	Leu	Met	Gly	Met	Leu	Ser	Thr	Ser	Leu	Ala	Asp	Gln
				325					330					335
Ile	Phe	Asn	Ala	Val	Ile	Lys	Gln	Asn	Pro	Phe	Leu	Val	Tyr	Gln
			340					345					350	
Pro	Cys	Phe	Trp	Asn	Val	Gln	Leu	Ser	Asp	His	Thr	Arg	Ser	Glu
			355				360					365		
Cys	Tyr	Arg	Asp	Val	Ser	Asp	Leu	Lys	Val	Ile	His	Trp	Asn	Ser
370							375					380		Pro
Lys	Lys	Leu	Arg	Val	Lys	Asn	Lys	His	Val	Glu	Phe	Phe	Arg	Asn
385							390					395		400
Tyr	Leu	Thr	Phe	Leu	Glu	Tyr	Asp	Gly	Asn	Leu	Leu	Arg	Arg	Glu
				405					410					415
Phe	Gly	Cys	Pro	Ser	Glu	Ala	Asp	Val	Asn	Ser	Glu	Asn	Leu	Gln
			420					425					430	Lys
Gln	Leu	Ser	Glu	Leu	Asp	Glu	Asp	Asp	Leu	Cys	Tyr	Glu	Phe	Arg
			435				440					445		Arg
Glu	Arg	Phe	Thr	Val	His	Arg	Thr	His	Leu	Tyr	Phe	Leu	His	Tyr
			450				455					460		Glu
Tyr	Glu	Pro	Ala	Ala	Asp	Ser	Thr	Asp	Val	Thr	Leu	Val	Ala	Gln
465							470					475		480
Ser	Met	Asp	Arg	Leu	Gln	Met	Leu	Glu	Ala	Ile	Cys	Lys	His	Trp
				485					490					495
Gly	Pro	Ile	Ser	Leu	Ala	Leu	Tyr	Leu	Ser	Asp	Ala	Glu	Ala	Gln
			500					505					510	
Phe	Leu	Arg	Tyr	Ala	Gln	Gly	Ser	Glu	Val	Leu	Met	Ser	Arg	His
			515				520					525		Asn
Val	Gly	Tyr	His	Ile	Val	Tyr	Lys	Glu	Gly	Gln	Phe	Tyr	Pro	Val
			530				535					540		Asn
Leu	Leu	Arg	Asn	Val	Ala	Met	Lys	His	Ile	Ser	Thr	Pro	Tyr	Met
545							550					555		560
Leu	Ser	Asp	Ile	Asp	Phe	Leu	Pro	Met	Tyr	Gly	Leu	Tyr	Glu	Tyr
				565					570				575	Leu
Arg	Lys	Ser	Val	Ile	Gln	Leu	Asp	Leu	Ala	Asn	Thr	Lys	Lys	Ala
														Met

580	585	590
Ile Val Pro Ala Phe Glu Thr Leu Arg Tyr Arg Leu Ser Phe Pro Lys 595	600	605
Ser Lys Ala Glu Leu Leu Ser Met Leu Asp Met Gly Thr Leu Phe Thr 610	615	620
Phe Arg Tyr His Val Trp Thr Lys Gly His Ala Pro Thr Asn Phe Ala 625	630	635
Lys Trp Arg Thr Ala Thr Thr Pro Tyr Arg Val Glu Trp Glu Ala Asp 645	650	655
Phe Glu Pro Tyr Val Val Val Arg Arg Asp Cys Pro Glu Tyr Asp Arg 660	665	670
Arg Phe Val Gly Phe Gly Trp Asn Lys Val Ala His Ile Met Glu Leu 675	680	685
Asp Val Gln Glu Tyr Glu Phe Ile Val Leu Pro Asn Ala Tyr Met Ile 690	695	700
His Met Pro His Ala Pro Ser Phe Asp Ile Thr Lys Phe Arg Ser Asn 705	710	715
Lys Gln Tyr Arg Ile Cys Leu Lys Thr Leu Lys Glu Glu Phe Gln Gln 725	730	735
Asp Met Ser Arg Arg Tyr Gly Phe Ala Ala Leu Lys Tyr Leu Thr Ala 740	745	750
Glu Asn Asn Ser 755		

(2) INFORMATION FOR SEQ ID NO:143:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1435 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

TGCACCGGTG GTCGGCTGTT GGGTGTGGAG TTTCCCAGCG CCCCTCGGGT CCGACCCCTTT	60
GAGCGTTCTG CTCCGGCGCC AGCCTACCTC GTCCTCGGC GCCATGACCA CAACCACCAC	120
CTTCAAGGGA GTCGACCCCA ACAGCAGGAA TAGCTCCCGA GTTTTGCGGC CTCCAGGTGG	180
TGGATCCAAT TTTTCATTAG GTTTTGATGA ACCAACAGAA CAACCTGTGA GGAAGAACAA	240

AATGGCCTCT AATATCTTTG GGACACCTGA AGAAAATCAA GCTTCTTGGG CCAAGTCAGC	300
AGGTGCCAAG TCTAGTGGTG GCAGGGAAGA CTTGGAGTCA TCTGGACTGC AGAGAAGGAA	360
CTCCTCTGAA GCAAGCTCCG GAGACTTCTT AGATCTGAAG GGAGAAGGTG ATATTCATGA	420
AAATGTGGAC ACAGACTTGC CAGGCAGCCT GGGGCAGAGT GAAGAGAAGC CCGTGCCTGC	480
TGCGCCTGTG CCCAGCCCGG TGGCCCCGGC CCCAGTGCCA TCCAGAAGAA ATCCCCCTGG	540
CGGCAAGTCC AGCCTCGTCT TGGGTTAGCT CTGACTGTCC TGAACGCTGT CGTTCTGTCT	600
GTTTCCTCCA TGCTTGTGAA CTGCACAACT TGAGCCTGAC TGTACATCTC TTGGATTGTG	660
TTCATTAAAA AGAAGCACTT TATGTACTGC TGTCTTTTTT TTTTTTCTT TTGAAGAACA	720
GGTTTCTCTC TGTCTTGAC TCTTGGGTCT GTGGGCCATG GCATGAGTGT TTTCTAGTAG	780
TAGATTGGAG GGAAAGCTTT GTGACACTTA GTACTGTGTT TTTAAGAAGA AATAATTGG	840
TTCCAGATGT GTTAGAGGAT CTTTTGTACT GAGGTTTTTA ACACCTTACT TGGGTTTACC	900
AAGCCTCAAC TGGACAGACC ATAAACAGTC CACAGGCACC GTTCCTGCCA GGCCCCAACC	960
CACAGGGAGT CTCTCCGAG AGCCTTCTTG GTGTTGCCCT AACTTGCCAG TGGCCTTTGC	1020
TCAGAGCCTC CTCCTGTGAC ATGTGAACAA TGAAGAGGCC TGCGCYTCCT GCCTTGCCGC	1080
CTGCAAAGCA AAGAACTGC CTTTTATTTT TTAACCTTAA AAAGTAGCCA GATAGTAACA	1140
AGACTGGCTG GCTGATGAGC AAAGCYTTTG CTCTCACGCA GAGGAAGGCT TGGATGTACA	1200
ATGAAACTGC CTGGAATAA AAGCAGTGAA GCAAGGGAGG CAATCACACT GAAGCGGGTC	1260
TTCTCCAGG AACGGGTCC CACAGGCGTG TTGTTTTAAA TAACCTGATG CTGTGTGCAT	1320
GATGCTGGTG CTTGACCATG AAAGGAAAGT CTCATCCTTA AAATGTGTTG TACTTCACAA	1380
TCCTGGACTG TTGCTTCAAG TAAACAATAT CCACATTTTG AAAAAAAAAA AAAAA	1435

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

Met Thr Thr Thr Thr Thr Phe Lys Gly Val Asp Pro Asn Ser Arg Asn

1	5	10	15
Ser Ser Arg Val Leu Arg Pro Pro Gly Gly Gly Ser Asn Phe Ser Leu			
20	25	30	
Gly Phe Asp Glu Pro Thr Glu Gln Pro Val Arg Lys Asn Lys Met Ala			
35	40	45	
Ser Asn Ile Phe Gly Thr Pro Glu Glu Asn Gln Ala Ser Trp Ala Lys			
50	55	60	
Ser Ala Gly Ala Lys Ser Ser Gly Gly Arg Glu Asp Leu Glu Ser Ser			
65	70	75	80
Gly Leu Gln Arg Arg Asn Ser Ser Glu Ala Ser Ser Gly Asp Phe Leu			
85	90	95	
Asp Leu Lys Gly Glu Gly Asp Ile His Glu Asn Val Asp Thr Asp Leu			
100	105	110	
Pro Gly Ser Leu Gly Gln Ser Glu Glu Lys Pro Val Pro Ala Ala Pro			
115	120	125	
Val Pro Ser Pro Val Ala Pro Ala Pro Val Pro Ser Arg Arg Asn Pro			
130	135	140	
Pro Gly Gly Lys Ser Ser Leu Val Leu Gly			
145	150		

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1904 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

CAGCGTCGCG CGCGCTACCA CACCCAGGTT CGGCCCGTAG GCGTCTGGCA GCCCGGCGCC	60
ATCTTCATCG AGCGCCATGG CCGCAGCCTG CGGGCCGGGA GCGGCCGGGT ACTGCTTGCT	120
CCTCGGCTTG CATTTGTTTC TGCTGACCGC GGGCCCTGCC CTGGGCTGGA ACGACCTGA	180
CAGAATGTTG CTGCGGGATG TAAAAGCTCT TACCCTCCAC TATGACCGCT ATACCACCTC	240
CCGCAGGCTG GATCCCATCC CACAGTTGAA ATGTGTTGGA GGCACAGCTG GTTGTGATTC	300
TTATACCCCA AAAGTCATAC AGTGTCAGAA CAAAGGCTGG GATGGGTATG ATGTACAGTG	360
GGAATGTAAG ACGGACTTAG ATATTGCATA CAAATTTGGA AAAACTGTGG TGAGCTGTGA	420

AGGCTATGAG TCCTCTGAAG ACCAGTATGT ACTAAGAGGT TCTTGTGGCT TGGAGTATAA	480
TTTAGATTAT ACAGAACTTG GCCTGCAGAA ACTGAAGGAG TCTGGAAAGC AGCACGGCTT	540
TGCCTCTTTC TCTGATTATT ATTATAAGTG GTCCTCGGCG GATTCCTGTA ACATGAGTGG	600
ATTGATTACC ATCGTGGTAC TCCTTGGGAT CGCCTTTGTA GTCTATAAGC TGTTCTGAG	660
TGACGGGCAG TATTCTCCTC CACCGTACTC TGAGTATCCT CCATTTTCCC ACCGTTACCA	720
GAGATTCACC AACTCAGCAG GACCTCCTCC CCCAGGCTTT AAGTCTGAGT TCACAGGACC	780
ACAGAATACT GGCCATGGTG CAACTTCTGG TTTTGGCAGT GCTTTTACAG GACAACAAGG	840
ATATGAAAAT TCAGGACCAG GGTTCCTGGAC AGGCTTGGGA ACTGGTGGAA TACTAGGATA	900
TTTGTTTGGC AGCAATAGAG CGGCAACACC CTTCTCAGAC TCGTGGTACT ACCCGTCTTA	960
TCCTCCCTCC TACCCTGGCA CGTGGAATAG GGCTTACTCA CCCCTTCATG GAGGCTCGGG	1020
CAGCTATTCG GTATGTTCAA ACTCAGACAC GAAAACCAGA ACTGCATCAG GATATGGTGG	1080
TACCAGGAGA CGATAAAGTA GAAAGTTGGA GTCAAACACT GGATGCAGAA ATTTTGGATT	1140
TTTCATCACT TTCTCTTAG AAAAAAAGTA CTACCTGTTA ACAATTGGGA AAAGGGGATA	1200
TTCAAAAGTT CTGTGGTGTT ATGTCCAGTG TAGCTTTTGG TATTCTATTA TTTGAGGCTA	1260
AAAGTTGATG TGTGACAAA TACTTATGTG TTGTATGTCA GTGTAACATG CAGATGTATA	1320
TTGCAGTTTT KGAAAGTGAT CATTACTGTG GAATGCTAAA AATACATTAA TTTCTAAAC	1380
CTGTGATGCC CTAAGAAGCA TTAAGAATGA AGGTGTTGTA CTAATAGAAA CTAAGTACAG	1440
AAAATTTAG TTTTAGGTGG TTGTAGCTGA TGAGTTATTA CCTCATAGAG ACTATAATAT	1500
TCTATTTGGT ATTATATTAT TTGATGTTTG CTGTTCTTCA AACATTTAAA TCAAGCTTTG	1560
GACTAATTAT GCTAATTTGT GAGTTCTGAT CACTTTTGAG CTCTGAAGCT TTGAATCATT	1620
CAGTGGTGGG GATGGCCTTC TGGTAACCTG ATATTACCTT CTGTAGGAAA AGGTGGAAAA	1680
TAAGCATCTA GAAGGTTGTT GTGAATGACT CTGTGCTGGC AAAAATGCTT GAAACCTCTA	1740
TATTTCTTTC GTTCATAAGA GGTAAAGGTC AAATTTTCA ACAAAGTCT TTTAATAACA	1800
AAAGCATGCA GTTCTCTGTG AAATCTCAAA TATTGTTGTA ATAGTCTGTT TCAATCTTAA	1860
AAAGAATCAA TAAAAACAAA CAAGGAAAAA AAAAAAAAAA AAAA	1904

(2) INFORMATION FOR SEQ ID NO:146:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 339 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:



(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

Met	Ala	Ala	Ala	Cys	Gly	Pro	Gly	Ala	Ala	Gly	Tyr	Cys	Leu	Leu	Leu		
1				5					10					15			
Gly	Leu	His	Leu	Phe	Leu	Leu	Thr	Ala	Gly	Pro	Ala	Leu	Gly	Trp	Asn		
			20					25					30				
Asp	Pro	Asp	Arg	Met	Leu	Leu	Arg	Asp	Val	Lys	Ala	Leu	Thr	Leu	His		
		35					40					45					
Tyr	Asp	Arg	Tyr	Thr	Thr	Ser	Arg	Arg	Leu	Asp	Pro	Ile	Pro	Gln	Leu		
	50					55					60						
Lys	Cys	Val	Gly	Gly	Thr	Ala	Gly	Cys	Asp	Ser	Tyr	Thr	Pro	Lys	Val		
65					70					75					80		
Ile	Gln	Cys	Gln	Asn	Lys	Gly	Trp	Asp	Gly	Tyr	Asp	Val	Gln	Trp	Glu		
				85					90					95			
Cys	Lys	Thr	Asp	Leu	Asp	Ile	Ala	Tyr	Lys	Phe	Gly	Lys	Thr	Val	Val		
			100					105					110				
Ser	Cys	Glu	Gly	Tyr	Glu	Ser	Ser	Glu	Asp	Gln	Tyr	Val	Leu	Arg	Gly		
		115					120					125					
Ser	Cys	Gly	Leu	Glu	Tyr	Asn	Leu	Asp	Tyr	Thr	Glu	Leu	Gly	Leu	Gln		
	130					135					140						
Lys	Leu	Lys	Glu	Ser	Gly	Lys	Gln	His	Gly	Phe	Ala	Ser	Phe	Ser	Asp		
145					150					155					160		
Tyr	Tyr	Tyr	Lys	Trp	Ser	Ser	Ala	Asp	Ser	Cys	Asn	Met	Ser	Gly	Leu		
				165					170					175			
Ile	Thr	Ile	Val	Val	Leu	Leu	Gly	Ile	Ala	Phe	Val	Val	Tyr	Lys	Leu		
			180					185						190			
Phe	Leu	Ser	Asp	Gly	Gln	Tyr	Ser	Pro	Pro	Pro	Tyr	Ser	Glu	Tyr	Pro		
		195					200					205					
Pro	Phe	Ser	His	Arg	Tyr	Gln	Arg	Phe	Thr	Asn	Ser	Ala	Gly	Pro	Pro		
	210					215					220						
Pro	Pro	Gly	Phe	Lys	Ser	Glu	Phe	Thr	Gly	Pro	Gln	Asn	Thr	Gly	His		
225					230					235					240		
Gly	Ala	Thr	Ser	Gly	Phe	Gly	Ser	Ala	Phe	Thr	Gly	Gln	Gln	Gly	Tyr		
				245					250					255			
Glu	Asn	Ser	Gly	Pro	Gly	Phe	Trp	Thr	Gly	Leu	Gly	Thr	Gly	Gly	Ile		

260	265	270
Leu Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr Pro Phe Ser Asp		
275	280	285
Ser Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro Gly Thr Trp Asn		
290	295	300
Arg Ala Tyr Ser Pro Leu His Gly Gly Ser Gly Ser Tyr Ser Val Cys		
305	310	315
Ser Asn Ser Asp Thr Lys Thr Arg Thr Ala Ser Gly Tyr Gly Gly Thr		
325	330	335
Arg Arg Arg		

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

CTGTCTGGCG GCGGCAGCAT GCGGCGGGG GCGGCTGAGG CAGCTGTAGC GGCCGTGGAG	60
GAGGTCGGCT CAGCCGGGCA GTTTGAGGAG CTGCTGCGCC TCAAAGCCAA GTCCCTCCTT	120
GTGGTCCATT TCTGGGCACC ATGGGCTCCA CAGTGTGCAC AGATGAACGA AGTTATGGCA	180
GAGTTAGCTA AAGAACTCCC TCAAGTTTCA TTTGTGAAGT TGGAAGCTGA AGGTGTTCTT	240
GAAGTATCTG AAAAATATGA AATTAGCTCT GTTCCCACTT TTCTGTTTTT CAAGAATTCT	300
CAGAAAATCG ACCGATTAGA TGGTGCACAT GCCCCAGAGT TGACCAAAAA AGTTCAGCGA	360
CATGCATCTA GTGGCTCCTT CCTACCCAGC GCTAATGAAC ATCTTAAAGA AGACCTCAGC	420
CTTCGCCTGA AAAAGCTGAC TCACGCTGCC CCCTGCATGC TGTTTCATGAA GGGAACACCT	480
CAAGAACCAC GCTGTGGTTT CAGCAAGCAG ATGGTGGAAG TCCTTCACAA ACACAATATT	540
CAGTTCAGCA GCTTTGATAT CTTCTCAGAT GAAGAAGTTC GACAGGGGCT CAAAACGTAC	600
TCTAATTGGC CCACCTATCC TCAGCTCTAT GTTTCTGGAG AGCTAATAGG AGGACTTGAC	660
ATAATTAAGG AGCTGGAAGC ATCAGAAGAG CTGGACACGA TCTGTCCCAA AGCTCCCAA	720
TTAGAGGAAA GGCTCAAAGT GCTGACAAAT AAAGCTTCTG TGATGCTCTT TATGAAAGGA	780

AACAAACAGG AAGCAAAATG TGGATTCAGC AAACAAATTC TGGAAATACT AAATAGTACT 840  
GGTGTGTAAT ATGAAACATT CGATATATTG GAGGATGAAG AAGTTCGGCA AGGATTAAAA 900  
GCTTACTCAA ATTGGCCAAC ATACCCTCAG CTGTATGTGA AAGGGGAGCT GGTGGGAGGA 960  
TTGGATATTG TGAAGGAACT GAAAGAAAAT GGTGAATTGC TGCCTATACT GAGAGGAGAA 1020  
AATTAATAAA TCTTAAACTT GGTGCCCAAC TATTGTAAGA AATATTTAAT TACATTGGGA 1080  
GCAGTTCATG ATTTAGTCCT CAGAAATGGA CTAGGAATAG AAAATTCCTG CTTTCTCAGT 1140  
TACATGTTTT GTGTATTTCA CAATGTCGTG CTAAATAAAT GTATGTTACA TTTTTTCCC 1200  
ACCAAAAATA GAATGCAATA AACATCTTCA AATTATTAAC AATAAAAAAA AAAAAAAAAA 1260

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

Met	Ala	Ala	Gly	Ala	Ala	Glu	Ala	Ala	Val	Ala	Ala	Val	Glu	Glu	Val
1			5						10					15	
Gly	Ser	Ala	Gly	Gln	Phe	Glu	Glu	Leu	Leu	Arg	Leu	Lys	Ala	Lys	Ser
			20					25					30		
Leu	Leu	Val	Val	His	Phe	Trp	Ala	Pro	Trp	Ala	Pro	Gln	Cys	Ala	Gln
		35					40					45			
Met	Asn	Glu	Val	Met	Ala	Glu	Leu	Ala	Lys	Glu	Leu	Pro	Gln	Val	Ser
	50					55					60				
Phe	Val	Lys	Leu	Glu	Ala	Glu	Gly	Val	Pro	Glu	Val	Ser	Glu	Lys	Tyr
65					70					75				80	
Glu	Ile	Ser	Ser	Val	Pro	Thr	Phe	Leu	Phe	Phe	Lys	Asn	Ser	Gln	Lys
				85					90					95	
Ile	Asp	Arg	Leu	Asp	Gly	Ala	His	Ala	Pro	Glu	Leu	Thr	Lys	Lys	Val
			100				105						110		
Gln	Arg	His	Ala	Ser	Ser	Gly	Ser	Phe	Leu	Pro	Ser	Ala	Asn	Glu	His
			115				120						125		

Leu	Lys	Glu	Asp	Leu	Ser	Leu	Arg	Leu	Lys	Lys	Leu	Thr	His	Ala	Ala	
130						135					140					
Pro	Cys	Met	Leu	Phe	Met	Lys	Gly	Thr	Pro	Gln	Glu	Pro	Arg	Cys	Gly	
145					150					155					160	
Phe	Ser	Lys	Gln	Met	Val	Glu	Ile	Leu	His	Lys	His	Asn	Ile	Gln	Phe	
				165					170					175		
Ser	Ser	Phe	Asp	Ile	Phe	Ser	Asp	Glu	Glu	Val	Arg	Gln	Gly	Leu	Lys	
			180					185					190			
Thr	Tyr	Ser	Asn	Trp	Pro	Thr	Tyr	Pro	Gln	Leu	Tyr	Val	Ser	Gly	Glu	
	195						200					205				
Leu	Ile	Gly	Gly	Leu	Asp	Ile	Ile	Lys	Glu	Leu	Glu	Ala	Ser	Glu	Glu	
210					215					220						
Leu	Asp	Thr	Ile	Cys	Pro	Lys	Ala	Pro	Lys	Leu	Glu	Glu	Arg	Leu	Lys	
225					230					235					240	
Val	Leu	Thr	Asn	Lys	Ala	Ser	Val	Met	Leu	Phe	Met	Lys	Gly	Asn	Lys	
				245					250					255		
Gln	Glu	Ala	Lys	Cys	Gly	Phe	Ser	Lys	Gln	Ile	Leu	Glu	Ile	Leu	Asn	
			260					265					270			
Ser	Thr	Gly	Val	Glu	Tyr	Glu	Thr	Phe	Asp	Ile	Leu	Glu	Asp	Glu	Glu	
		275					280					285				
Val	Arg	Gln	Gly	Leu	Lys	Ala	Tyr	Ser	Asn	Trp	Pro	Thr	Tyr	Pro	Gln	
	290					295					300					
Leu	Tyr	Val	Lys	Gly	Glu	Leu	Val	Gly	Gly	Leu	Asp	Ile	Val	Lys	Glu	
305					310					315					320	
Leu	Lys	Glu	Asn	Gly	Glu	Leu	Leu	Pro	Ile	Leu	Arg	Gly	Glu	Asn		
				325					330					335		

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

ACTTTTGTGCG ATGCCTACTG GAGACTTTGA TTCGAAGCCC AGTTGGGCCG ACCAGGTGGA	60
GGAGGAGGGG GAGGACGACA AATGTGTCAC CAGCGAGCTC CTCAAGGGGA TCCCTCTGGC	120

CACAGGTGAC	ACCAGCCCAG	AGCCAGAGCT	ACTGCCGGGA	GCTCCACTGC	CGCCTCCCAA	180
GGAGGTCATC	AACGGAAACA	TAAAGACAGT	GACAGAGTAC	AAGATAGATG	AGGATGGCAA	240
GAAGTTCAAG	ATTGTCCGCA	CCTTCAGGAT	TGAGACCCGG	AAGGCTTCAA	AGGCTGTCTC	300
AAGGAGGAAG	AACTGGAAGA	AGTTCGGGAA	CTCAGAGTTT	GACCCCCCCG	GACCCAATGT	360
GGCCACCACC	ACTGTCAGTG	ACGATGTCTC	TATGACGTTC	ATCACCAGCA	AAGAGGACCT	420
GAACTGCCAG	GAGGAGGAGG	ACCCTATGAA	CAAACCTCAAG	GGCCAGAAGA	TCGTGTCCTG	480
CCGCATCTGC	AAGGGCGACC	ACTGGACCAC	CCGCTGCCCC	TACAAGGATA	CGCTGGGGCC	540
CATGCAGAAG	GAGCTGGCCG	AGCAGCTGGG	CCTGTCTACT	GGCGAGAAGG	AGAAGCTGCC	600
GGGAGAGCTA	GAGCCGGTGC	AGGCCACGCA	GAACAAGACA	GGGAAGTATG	TGCCGCCGAG	660
CCTGCGCGAC	GGGGCCAGCC	GCCGCGGGGA	GTCCATGCAG	CCCACCCGCA	GAGCCGACGA	720
CAACGCCACC	ATCCGTGTCA	CCAAC TTGTC	AGAGGACACG	CGTGAGACCG	ACCTGCAGGA	780
GCTCTTCCGG	CCTTTCGGCT	CCATCTCCCG	CATCTACCTG	GCTAAGGACA	AGACCACTGG	840
CCAATCCAAG	GGCTTCGCCT	TCATCAGCTT	CCACCGCCGC	GAGGATGCTG	CGCGTGCCAT	900
TGCCGGGGTG	TCCGGCTTTG	GCTACGACCA	CCTCATCCTC	AACGTCGAGT	GGGCCAAGCC	960
GTCCACCAAC	TAAGCCAGCT	GCCACCGTGT	ACTCGGTCCG	GGACCCCTTG	CGACAGAAGA	1020
CAGCCTCCGA	GAGCGCGGGC	TCCAAGGGCA	ATAAAGCAGC	TCCACTCTCA	AAAAAAAAAA	1080
AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	1140
AAAAAAAAAA	AA					1152

(2) INFORMATION FOR SEQ ID NO:150:

## (ii) MOLECULE TYPE: protein

Met	Pro	Thr	Gly	Asp	Phe	Asp	Ser	Lys	Pro	Ser	Trp	Ala	Asp	Gln	Val
1				5					10					15	
Glu	Glu	Glu	Gly	Glu	Asp	Asp	Lys	Cys	Val	Thr	Ser	Glu	Leu	Leu	Lys
			20					25					30		

Gly	Ile	Pro	Leu	Ala	Thr	Gly	Asp	Thr	Ser	Pro	Glu	Pro	Glu	Leu	Leu	35	40	45	
Pro	Gly	Ala	Pro	Leu	Pro	Pro	Pro	Lys	Glu	Val	Ile	Asn	Gly	Asn	Ile	50	55	60	
Lys	Thr	Val	Thr	Glu	Tyr	Lys	Ile	Asp	Glu	Asp	Gly	Lys	Lys	Phe	Lys	65	70	75	80
Ile	Val	Arg	Thr	Phe	Arg	Ile	Glu	Thr	Arg	Lys	Ala	Ser	Lys	Ala	Val	85	90	95	
Ala	Arg	Arg	Lys	Asn	Trp	Lys	Lys	Phe	Gly	Asn	Ser	Glu	Phe	Asp	Pro	100	105	110	
Pro	Gly	Pro	Asn	Val	Ala	Thr	Thr	Thr	Val	Ser	Asp	Asp	Val	Ser	Met	115	120	125	
Thr	Phe	Ile	Thr	Ser	Lys	Glu	Asp	Leu	Asn	Cys	Gln	Glu	Glu	Glu	Asp	130	135	140	
Pro	Met	Asn	Lys	Leu	Lys	Gly	Gln	Lys	Ile	Val	Ser	Cys	Arg	Ile	Cys	145	150	155	160
Lys	Gly	Asp	His	Trp	Thr	Thr	Arg	Cys	Pro	Tyr	Lys	Asp	Thr	Leu	Gly	165	170	175	
Pro	Met	Gln	Lys	Glu	Leu	Ala	Glu	Gln	Leu	Gly	Leu	Ser	Thr	Gly	Glu	180	185	190	
Lys	Glu	Lys	Leu	Pro	Gly	Glu	Leu	Glu	Pro	Val	Gln	Ala	Thr	Gln	Asn	195	200	205	
Lys	Thr	Gly	Lys	Tyr	Val	Pro	Pro	Ser	Leu	Arg	Asp	Gly	Ala	Ser	Arg	210	215	220	
Arg	Gly	Glu	Ser	Met	Gln	Pro	Thr	Arg	Arg	Ala	Asp	Asp	Asn	Ala	Thr	225	230	235	240
Ile	Arg	Val	Thr	Asn	Leu	Ser	Glu	Asp	Thr	Arg	Glu	Thr	Asp	Leu	Gln	245	250	255	
Glu	Leu	Phe	Arg	Pro	Phe	Gly	Ser	Ile	Ser	Arg	Ile	Tyr	Leu	Ala	Lys	260	265	270	
Asp	Lys	Thr	Thr	Gly	Gln	Ser	Lys	Gly	Phe	Ala	Phe	Ile	Ser	Phe	His	275	280	285	
Arg	Arg	Glu	Asp	Ala	Ala	Arg	Ala	Ile	Ala	Gly	Val	Ser	Gly	Phe	Gly	290	295	300	
Tyr	Asp	His	Leu	Ile	Leu	Asn	Val	Glu	Trp	Ala	Lys	Pro	Ser	Thr	Asn	305	310	315	320

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1594 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

CTGAGACCTG GGCTGCTGTG AAAGCCCCTG CACAATCAGC CAGGGAGAAC TGGGCGGGTT	60
TAGTGGCCCC AGGCCCCTC CTCATGCAGC AGTGTGCTGG GGCACAGCT CGTCTCCCCT	120
CTCTTAAGCA CCCGCTTCCT CACCACCCCC ACTGTTGGGC CTATAGTAGC AGGTTAGTGA	180
GTACCTAGGG CGGCTCAACT CCTCCACAG CACCAACCCA GCATGGTCCC ACTGAAGTCC	240
TACTACGCCC TCCCCTCCCC AGCCTTTTCC AGAAACCATA CTGGGCTCAG ATCAGAGCTC	300
CGAAGCGGTC AAAGTGAGCT GAGCAGGACA GGCCAGCCT TTCTCCACTG CCACGTCCCT	360
CATGCACATC ACTCATCTCC TGCTGCAGGC CAAGGCCAAA ATTGGGCTAG TCCTGGCCAG	420
GGAAATCAGA AGCTCTTCTT GGGTGAGATT GAGCCTCCTG TTGCTCCCTG GAGTTCCGGA	480
GGCTGGGCTG CAGCCCCTC AGCTTGCGGG CAAAATACGT GCTCTCCTCT CTCCTTGTC	540
GCTGAGCAAA CCCAGGGAAT AGCCCTCCTC TCCCAGGAA ACTTCTCTGA AATCTTAGAC	600
TTAGCCAGTC TTAGGCCTAC GATGCCACAC AAAGGTTGTT CAGGGAGAAG GGGGTGCAGG	660
AGGCAGAGGG TGCCCCGAG GGAGCTGGTG GCTCCAGCCC CACTAGAGCT CCTAAAGATC	720
ACACAGCAGC TGCTCCTGAC AGGGATGCTC ATGCCAGAA AGCAAGCCCA GGAGAGGAAG	780
GCAGAGTGTG ACAGAGCAGA GCCAGGGCCA GGCGCACCAG GAGAGGCGTT TCTGGGGCTC	840
CAGGGAAGTG CCACGGGAGG CAGAAGTCCA GAACTGCCCA TATAGATGCC CTTCTACATC	900
CTGGAGCCCA AATCAGTCAT GTGGGTGGGA AGTTCCCAGG GCAGTGGTCA CATCGTGAGA	960
ATTAGCAGGA AAGGCGGGGC CTTTCTTGTC ATAGCTATTT CTGAGGATGA AATGGGAGAC	1020
ATATGCCCAG CACCTGATGT AAGTTTATAT AATGTACCTA CCACTAAGAA ATACATGAAC	1080
CGTGCCATGA GGACAGTAAG TGTTCAATAA GCAACATGAA GCAAGAAACA GTGCAGGGTG	1140
CCCAGTGCAC AACTAGAGA GAAATTGTGA ACATTAAGGA CAAGGAGAAT TGGTGTCTTT	1200
CTAAACATA CTTATTTAAA AACACATACC CACTTACTAA TGTGGAATTA CACAGTTTGT	1260
AACAAGAAAA CAGTCTCTCC CATTCTCTAG TACTGYTCCC CTACCCAGCA GTCAMTTCCA	1320
GTTCAATCAG STATTTTAA AATGTGCTTA TATGACTCTT GCTTGATATA TCAATYTTAG	1380

ACATTACCTG TTGACTCCCT GTTGTGCATAC ATGAGGCTTT AGCTCTYTTT TGTCAGCAAC 1440  
 CCTCCCCCAT CCCTAGTTAT TAGGTTAAAA AATACTCAGA TTACTATTTC TATTACTATG 1500  
 TGAAAGTTAA CTGCGGAGCC AAGAGTTGGA CTATAATTAA ATTACCTTCC TTGTAAAAAA 1560  
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAA 1594

(2) INFORMATION FOR SEQ ID NO:152:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 220 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

Met	Val	Pro	Leu	Lys	Ser	Tyr	Tyr	Ala	Leu	Pro	Ser	Pro	Ala	Phe	Ser	1	5	10	15
Arg	Asn	His	Thr	Gly	Leu	Arg	Ser	Glu	Leu	Arg	Ser	Gly	Gln	Ser	Glu	20	25	30	
Leu	Ser	Arg	Thr	Gly	Pro	Ala	Phe	Leu	His	Cys	His	Val	Pro	His	Ala	35	40	45	
His	His	Ser	Ser	Pro	Ala	Ala	Gly	Gln	Gly	Gln	Asn	Trp	Ala	Ser	Pro	50	55	60	
Gly	Gln	Gly	Asn	Gln	Lys	Leu	Phe	Leu	Gly	Glu	Ile	Glu	Pro	Pro	Val	65	70	75	80
Ala	Pro	Trp	Ser	Ser	Gly	Gly	Trp	Ala	Ala	Ala	His	Ser	Ala	Cys	Gly	85	90	95	
Gln	Asn	Thr	Cys	Ser	Pro	Leu	Ser	Leu	Ser	Ala	Glu	Gln	Thr	Gln	Gly	100	105	110	
Ile	Ala	Leu	Leu	Ser	Pro	Gly	Asn	Phe	Ser	Glu	Ile	Leu	Asp	Leu	Ala	115	120	125	
Ser	Leu	Arg	Pro	Thr	Met	Pro	His	Lys	Gly	Cys	Ser	Gly	Arg	Arg	Gly	130	135	140	
Cys	Arg	Arg	Gln	Arg	Val	Pro	Arg	Arg	Glu	Leu	Val	Ala	Pro	Ala	Pro	145	150	155	160
Leu	Glu	Leu	Leu	Lys	Ile	Thr	Gln	Gln	Leu	Leu	Leu	Thr	Gly	Met	Leu	165	170	175	
Met	Pro	Arg	Lys	Gln	Ala	Gln	Glu	Arg	Lys	Ala	Glu	Cys	Asp	Arg	Ala	180	185	190	



Glu Pro Gly Pro Gly Ala Pro Gly Glu Ala Phe Leu Gly Leu Gln Gly  
195 200 205

Ser Ala Thr Gly Gly Arg Ser Pro Glu Leu Pro Ile  
210 215 220

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

TNAATAAACTG GACGGATGCA CTGATAGG

29

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

CNCTGATAACA AAGCATTGCC ACTGGCGC

29

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

TNATCCAGAAA ATTACCGCCG TCCGACCG

29

(2) INFORMATION FOR SEQ ID NO:156:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligonucleotide"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

CNCTTAGAAGC CTCATTTTG GGAAGTC

29

(2) INFORMATION FOR SEQ ID NO:157:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligonucleotide"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

CNGAGAAGACT CAACGAGGCA GCCAAGAA

29

(2) INFORMATION FOR SEQ ID NO:158:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligonucleotide"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

CNTGCTGACTT GGCCAAGAA GCTTGATT

29

(2) INFORMATION FOR SEQ ID NO:159:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

GNGCTGCTTTC CAGACTCCTT CAGTTTCT

29

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

ANCCACAGCGT GGTCTTGAG GTGTTCCC

29

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

GNTCTTCTGGC CCTTGAGTTT GTTCATAG

29

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

GNTGAGCCGCC CTAGGTACTC ACTAACCT

29

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1480 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

AGGCGCCCTC CCTTCCTGAG GAGCTGTTGG CCTGGGTGGG CAGGAACTGC AGTATGGCCA 60  
TGGGCTGAGC AGGCTGAGCA CCTCAGCCTT TAGGGCTTAT GGCCAGGGGA CACTGTATGA 120  
CTCTCCTCTC CTGCAGGTGT CTATCCACCT GGGGTATGGC ATCTACCGAC CTGTCTCCCT 180  
GGGGTCACAT GCTTTGTTTC CATTCTTGTC CTGGCTGGAC CAGCCACTGT GGGACCAACA 240  
CCCCCTCCAC ACTCCCCCAG ACTGCTCGTC TATCACCAGG ATCGCTTTGT ACTTTGTGCA 300  
AAAGGGTCTG GCTGTCCCTT GCTGTTTTCA TCTTGCCAA GCCTATTGTG CCTCTGGCTG 360  
CTGTATGTGT GCGCGTGCAC GTGTGTGTGT TTCATCTGTT CATTCACTGC ACAAGATATT 420  
TATTGAGTGC CCACTACGTG CCAGGCACTG TTGCTGAGTT CCTGTGGGTG TGTCTCTCGA 480  
TGCCACTCCT GCTTCTCTGG GGGCCTCTTT CTGTGCTTCT CTTTGTCCCC AAATTGCTAC 540  
CTCTTTGTCA GTCTGGGTGT CTCAGGTTCT GTGTGTCCTT GTGTGCATT CTGTCTCTCT 600  
CTGTCTCTGT CTCTCTGCAA GGCCCTCTAT TTCTCTCTTT CTTGGTGTCT GTCCTTTGCC 660  
CCCTGTGCCC TCTGGATTCT CTGGGTCTAT GTAGGCCCTT GGTCTGCCCT GGGCTCATCA 720  
GCCTTCCTGA CCTCCTCCTG CCCTCCCCCT CACTCCCTCC CTGGCTCTGC CAGTCGGTTC 780  
CCACGGAGCC ATTTTGTAGCT CTGATCAGCA TGGGAATGTG CCTCGGCCTC CAAGGGGCTT 840  
TGTCTGGTG CCCCCGCCCC TGGTCCCAAC CTGATCCCAC GAGGGAGTTG GGACAGGAGG 900  
ATTGATGGTG CTCCCTTCC TGCCAGCGTC AGAGGCCCTG GAGAGGGGCT GTCCATGGCA 960  
GCTGGTCTTT ATTCCTCCCT CATGAGCACA GGGTCGGGGG GTCCCCATTC TTGGAAGAGG 1020  
TTGAGAAGAC TCCTGGGCTT CAGCCTCTCC CACCCAGCCC TGCCCTCAC CTGCCTGCCC 1080  
TCCCCTCCCC CACTCTATAC TAGGACTGG ATCTCAGCCT CTGATCAGTT TCACAAAGTT 1140  
TGTTCCTAA GGAAATCAAA TCCCATTGTC ACCTAACTCT GAAGATCTAA ATAGCCCTTG 1200  
GATCAGTACG GGAACCCCAA ATCCCACAGG GCCAGATGTG GAGTCTGTGT CTGCCCCCGT 1260

CTTCTCTCCA TCCTCAAAGC CCCCACTTCT CTCCAGGCTG TTTCTTTTTT TATGACTGTA 1320  
AACATAGATA GTGCTTTTATT TTGTTAATAA TAAGATAATG ATGAGTAACT TAACCAGCAC 1380  
ATTTCTCCTG TTTACACTCG GGGGATTTTT TTGTTTCTG ATGACATAAT AAAGACAGAT 1440  
CATTTTCAGAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1480

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

Met	Ala	Arg	Gly	His	Cys	Met	Thr	Leu	Leu	Ser	Cys	Arg	Cys	Leu	Ser	1	5	10	15
Thr	Trp	Gly	Met	Ala	Ser	Thr	Asp	Leu	Ser	Pro	Trp	Gly	His	Met	Leu	20	25	30	
Cys	Phe	His	Ser	Cys	Pro	Gly	Trp	Thr	Ser	His	Cys	Gly	Thr	Asn	Thr	35	40	45	
Pro	Pro	Thr	Leu	Pro	Gln	Thr	Ala	Arg	Leu	Ser	Pro	Gly	Ser	Leu	Cys	50	55	60	
Thr	Leu	Cys	Lys	Arg	Val	Trp	Leu	Ser	Leu	Ala	Val	Phe	Ile	Ser	Ala	65	70	75	80
Lys	Pro	Ile	Val	Pro	Leu	Ala	Ala	Val	Cys	Val	Arg	Val	His	Val	Cys	85	90	95	
Val	Phe	His	Leu	Phe	Ile	His	Cys	Thr	Arg	Tyr	Leu	Leu	Ser	Ala	His	100	105	110	
Tyr	Val	Pro	Gly	Thr	Val	Ala	Glu	Phe	Leu	Trp	Val	Cys	Leu	Ser	Met	115	120	125	
Pro	Leu	Leu	Leu	Leu	Trp	Gly	Pro	Leu	Ser	Val	Leu	Leu	Phe	Val	Pro	130	135	140	
Lys	Leu	Leu	Pro	Leu	Cys	Gln	Ser	Gly	Cys	Leu	Arg	Phe	Cys	Val	Ser	145	150	155	160
Leu	Cys	Ala	Phe	Leu	Ser	Leu	Ser	Val	Leu	Val	Ser	Leu	Gln	Gly	Pro	165	170	175	
Leu	Phe	Leu	Ser	Phe	Leu	Val	Ser	Val	Leu	Cys	Pro	Leu	Cys	Pro	Leu				

180	185	190
Asp Ser Leu Gly Leu Cys Arg	Pro Leu Val Cys Pro Gly Leu Ile Ser	
195	200	205
Leu Pro Asp Leu Leu Leu Pro Ser Pro Ser Leu Pro Pro Trp Leu Cys		
210	215	220
Gln Ser Val Pro Thr Glu Pro Phe Leu Ala Leu Ile Ser Met Gly Met		
225	230	235
Cys Leu Gly Leu Gln Gly Ala Leu Ser Trp Cys Pro Arg Pro Trp Ser		
245	250	255
Gln Pro Asp Pro Thr Arg Glu Leu Gly Gln Glu Asp		
260	265	

(2) INFORMATION FOR SEQ ID NO:165:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1436 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

CCCGGCGGGCT CCTGGAACCC CGGTTTCGCGG CGATGCCAGC CACCCCAGCG AAGCCGCCGC	60
AGTTCAGTGC TTGGATAATT TGAAAGTACA ATAGTTGGTT TCCCTGTCCA CCCGCCCCAC	120
TTCGCTTGCC ATCACAGCAC GCCTATCGGA TGTGAGAGGA GAAGTCCCGC TGCTCGGGCA	180
CTGTCTATAT ACGCCTAACA CCTACATATA TTTTAAAAAC ATTAAATATA ATTAACAATC	240
AAAAGAAAGA GGAGAAAGGA AGGGAAGCAT TACTGGGTTA CTATGCACTT GCGACTGATT	300
TCTTGCGCTT TTATCATTTT GAACTTTATG GAATACATCG GCAGCCAAAA CGCCTCCCGG	360
GGAAGGCGCC AGCGAAGAAT GCATCCTAAC GTTAGTCAAG GCTGCCAAGG AGGCTGTGCA	420
ACATGCTCAG ATTACAATGG ATGTTTGTCA TGTAAGCCCA GACTATTTTT TGCTCTGGAA	480
AGAATTGGCA TGAAGCAGAT TGGAGTATGT CTCTCTTCAT GTCCAAGTGG ATATTATGGA	540
ACTCGATATC CAGATATAAA TAAGTGTAACA AAATGCAAAG CTGACTGTGA TACCTGTTTC	600
AACAAAAATT TCTGCACAAA ATGTAAAAGT GGATTTTACT TACACCTTGG AAAGTGCCTT	660
GACAATTGCC CAGAAGGGTT GGAAGCCAAC AACCATACTA TGGAGTGTGT CAGTATTGTG	720
CACTGTGAGG TCAGTGAATG GAATCCTTGG AGTCCATGCA CGAAGAAGGG AAAACATGT	780

GGCTTCAAAA GAGGGACTGA AACACGGGTC CGAGAAATAA TACAGCATCC TTCAGCAAAG 840  
GGTAACCTGT GTCCCCAAC AAATGAGACA AGAAAGTGTA CAGTGCAAAG GAAGAAGTGT 900  
CAGAAGGGAG AACGAGGAAA AAAAGGAAGG GAGAGGAAAA GAAAAAAACC TAATAAAGGA 960  
GAAAGTAAAG AAGCAATACC TGACAGCAAA AGTCTGGAAT CCAGCAAAGA AATCCCAGAG 1020  
CAACGAGAAA ACAAACAGCA GCAGAAGAAG CGAAAAGTCC AAGATAAACA GAAATCGGGG 1080  
ATTGAAGTCA CCCTAGCTGA AGGCCTCACC AGTGTTCAC AGAGGACACA GCCCACCCCT 1140  
TGCAGGAGGA GGTATCTCTG AGTGTGCAGC ACAGAATCGC ATGACCCACC TTAACCTTCC 1200  
TGTTGTCATG GAAGGATGCA CGGCTGCTCT GTCCACTGTG ATTCCTAGCC CTCTCAAGAT 1260  
CACTGCTTTC TGAAGAATTT GCAATGACTC TGGCTTCTGG CTGCTTATCT CTGGACACCC 1320  
GTTCTCCACC AGTTGTACAG TTCATGTAAT CTAATTGGCT TAATTGATTT TCCACTTCTC 1380  
TCTTCCTCTT CTAAGATATA AACATTTTAA ATGATTTAAA AAAAAAAAAA AAAAAA 1436

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

Met	His	Leu	Arg	Leu	Ile	Ser	Trp	Leu	Phe	Ile	Ile	Leu	Asn	Phe	Met
1				5					10					15	
Glu	Tyr	Ile	Gly	Ser	Gln	Asn	Ala	Ser	Arg	Gly	Arg	Arg	Gln	Arg	Arg
			20					25					30		
Met	His	Pro	Asn	Val	Ser	Gln	Gly	Cys	Gln	Gly	Gly	Cys	Ala	Thr	Cys
		35					40					45			
Ser	Asp	Tyr	Asn	Gly	Cys	Leu	Ser	Cys	Lys	Pro	Arg	Leu	Phe	Phe	Ala
	50				55						60				
Leu	Glu	Arg	Ile	Gly	Met	Lys	Gln	Ile	Gly	Val	Cys	Leu	Ser	Ser	Cys
65					70				75					80	
Pro	Ser	Gly	Tyr	Tyr	Gly	Thr	Arg	Tyr	Pro	Asp	Ile	Asn	Lys	Cys	Thr
			85					90					95		
Lys	Cys	Lys	Ala	Asp	Cys	Asp	Thr	Cys	Phe	Asn	Lys	Asn	Phe	Cys	Thr
		100					105						110		
Lys	Cys	Lys	Ser	Gly	Phe	Tyr	Leu	His	Leu	Gly	Lys	Cys	Leu	Asp	Asn

115	120	125
Cys Pro Glu Gly Leu Glu Ala Asn Asn His Thr Met Glu Cys Val Ser		
130	135	140
Ile Val His Cys Glu Val Ser Glu Trp Asn Pro Trp Ser Pro Cys Thr		
145	150	155
Lys Lys Gly Lys Thr Cys Gly Phe Lys Arg Gly Thr Glu Thr Arg Val		
165	170	175
Arg Glu Ile Ile Gln His Pro Ser Ala Lys Gly Asn Leu Cys Pro Pro		
180	185	190
Thr Asn Glu Thr Arg Lys Cys Thr Val Gln Arg Lys Lys Cys Gln Lys		
195	200	205
Gly Glu Arg Gly Lys Lys Gly Arg Glu Arg Lys Arg Lys Lys Pro Asn		
210	215	220
Lys Gly Glu Ser Lys Glu Ala Ile Pro Asp Ser Lys Ser Leu Glu Ser		
225	230	235
Ser Lys Glu Ile Pro Glu Gln Arg Glu Asn Lys Gln Gln Gln Lys Lys		
245	250	255
Arg Lys Val Gln Asp Lys Gln Lys Ser Gly Ile Glu Val Thr Leu Ala		
260	265	270
Glu Gly Leu Thr Ser Val Ser Gln Arg Thr Gln Pro Thr Pro Cys Arg		
275	280	285
Arg Arg Tyr Leu		
290		

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2322 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

GGTTAAGAGC AGATTAGAAC AGAAATCAGG AGAACTTGGG AAGAAGATCA CTGAGTTAAC	60
ATTGAAAAAT CAGACACTAC AAAAGGAAAT TGAAAAAGTT TATTTGGATA ATAAGCTCCT	120
CAAGGAGCAA GCACATAACT TAACAATTGA AATGAAAAAT CATTATGTTC CTTTAAAAGT	180
AAGTGAAGAC ATGAAAAAGT CACATGATGC AATTATTGAT GATCTTAATA GAAAGCTTTT	240



AGATGTAACA	CAAAAATATA	CAGAAAAGAA	GTTGGAAATG	GAGAAATTGC	TACTGGAAAA	300
TGACAGCTTA	AGTAAGGATG	TAAGCCGCCT	AGAAACTGTG	TTTGTACCTC	CTGAGAAACA	360
TGAAAAAGAG	ATAATAGCTC	TGAAATCCAA	TATTGTTGAA	CTTAAGAAAC	AGCTGTCTGA	420
ACTTAAGAAA	AAATGTGGTG	AAGACCAGGA	GAAAATACAC	GCTCTCACAT	CTGAAAACAC	480
TAACTTGAAG	AAGATGATGA	GTAATCAGTA	TGTGCCAGTT	AAAACCCATG	AAGAGGTTAA	540
AATGACACTG	AATGACACGT	TAGCCAAAAC	TAACAGAGAA	TTATTAGATG	TGAAGAAAAA	600
ATTTGAAGAT	ATAAATCAGG	AATTTGTAAA	AATAAAAGAT	AAGAATGAAA	TATTAAAAAG	660
AAACCTGGAA	AACACTCAGA	ACCAAATAAA	AGCTGAGTAC	ATCAGCCTGG	CAGAGCACGA	720
GGCAAAGATG	AGCTCGCTAA	GTCAGAGCAT	GAGAAAGGTG	CAGGATAGTA	ATGCTGAAAT	780
CTTGGCCAAC	TACAGAAAAG	GCCAAGAAGA	GATTGTGACA	CTGCATGCCG	AAATTAAAGC	840
CCAGAAGAAG	GAGCTCGACA	CAATACAAGA	ATGCATTAAG	GTAAAAATATG	CCCCAATTGT	900
CAGCTTTGAG	GAGTGCGAGA	GAAAATTTAA	AGCAACAGAG	AAAGAACTAA	AAGACCAGTT	960
ATCAGAGCAG	ACACAAAAGT	ATAGTGTCAG	TGAAGAAGAA	GTCAAGAAAA	ACAAGCAAGA	1020
GAATGACAAG	TTAAGAAGG	AGATTTTTAC	CCTTCAGAAA	GATTTGAGAG	ATAAGACAGT	1080
TCTCATTGAG	AAGTCTCATG	AAATGGAAAG	AGCATTAAAGC	AGAAAAACAG	ACGAGCTAAA	1140
CAAACAGTTA	AAAGACTTGT	CACAGAAATA	CACGGAAGTA	AAGAATGTGA	AAGAGAAGCT	1200
AGTAGAAGAA	AATGCCAAAC	AGACTTCTGA	GATACTTGCA	GTGCAAAATC	TTTTGCAAAA	1260
ACAACATGTT	CCATTGGAAC	AGGTTGAGGC	TCTGAAAAAA	TCTCTTAATG	GCACAATTGA	1320
AAATCTAAAG	GAAGAACTGA	AGAGTATGCA	AAGGTGTTAC	GAGAAAGAGC	AGCAGACAGT	1380
GACCAAACCTG	CATCAATTGT	TGGAGAAATCA	AAAGAACTCT	TCTGTACCCC	TGGCAGAGCA	1440
TTTGCAGATT	AAAGAAGCAT	TTGAGAAAGA	AGTTGGAATC	ATAAAAGCCA	GCTTGAGAGA	1500
AAAGGAAGAA	GAAAGCCAAA	ACAAAATGGA	AGAAGTCTCC	AACTTCAGT	CGGAGGTTCA	1560
GAATACTAAA	CAAGCATTA	AAAAATTAGA	GACTAGAGAG	GTAGTTGACT	TGTCTAAATA	1620
TAAAGCAACA	AAAAGTGATT	TGGAGACACA	GATTTCTAGC	TTAAATGAAA	AATTGGCCAA	1680
TCTGAATAGA	AAGTATGAGG	AAGTATGTGA	GGAAGTTTTG	CATGCCAAAA	AGAAGGAAAT	1740
ATCTGCAAAA	GATGAGAAGG	AATTACTGCA	TTTCAGCATT	GAGCAAGAAA	TTAAGGATCA	1800
GAAGGAACGA	TGTGATAAGT	CCTTAACAAC	AATCACAGAG	TTACAAAGAA	GAATACAAGA	1860
ATCTGCTAAA	CAAATAGAAG	CAAAAGATAA	TAAGATAACT	GAACTGCTTA	ATGATGTGGA	1920
AAGATTAAAA	CAGGCACTCA	ATGGCCTTTC	CCAACCTACC	TACACAAGTG	GGAACCCAC	1980

CAAGAGGCAG AGCCAGCTGA TTGACACTCT GCAGCACCAA GTGAAATCTC TGGAGCAACA 2040  
GCTGGCCGAT GCTGACAGAC AGCACCAAGA AGTAATTGCA ATTTATCGGA CACACCTTCT 2100  
TAGTGCTGCA CAGGGTCACA TGGATGAAGA TGTTCAGGAG GCTCTGCTCC AGATCATACA 2160  
AATGCGGCAG GGGCTTGTGT GCTAGCCGTT AGCACTGACT GCCAGTATCT GTTTTATCTT 2220  
GCTGGTGCTG AACATTCTTT GTGCAACTCC ATGGTCTTTC TGGGCCTTAC TGTGCTGGTA 2280  
TAATTAAAAT AAAATATATT TTGTTCTAAA AAAAAAAAAA AA 2322

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 677 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

Met	Lys	Asn	His	Tyr	Val	Pro	Leu	Lys	Val	Ser	Glu	Asp	Met	Lys	Lys	1	5	10	15
Ser	His	Asp	Ala	Ile	Ile	Asp	Asp	Leu	Asn	Arg	Lys	Leu	Leu	Asp	Val	20	25	30	
Thr	Gln	Lys	Tyr	Thr	Glu	Lys	Lys	Leu	Glu	Met	Glu	Lys	Leu	Leu	Leu	35	40	45	
Glu	Asn	Asp	Ser	Leu	Ser	Lys	Asp	Val	Ser	Arg	Leu	Glu	Thr	Val	Phe	50	55	60	
Val	Pro	Pro	Glu	Lys	His	Glu	Lys	Glu	Ile	Ile	Ala	Leu	Lys	Ser	Asn	65	70	75	80
Ile	Val	Glu	Leu	Lys	Lys	Gln	Leu	Ser	Glu	Leu	Lys	Lys	Lys	Cys	Gly	85	90	95	
Glu	Asp	Gln	Glu	Lys	Ile	His	Ala	Leu	Thr	Ser	Glu	Asn	Thr	Asn	Leu	100	105	110	
Lys	Lys	Met	Met	Ser	Asn	Gln	Tyr	Val	Pro	Val	Lys	Thr	His	Glu	Glu	115	120	125	
Val	Lys	Met	Thr	Leu	Asn	Asp	Thr	Leu	Ala	Lys	Thr	Asn	Arg	Glu	Leu	130	135	140	
Leu	Asp	Val	Lys	Lys	Lys	Phe	Glu	Asp	Ile	Asn	Gln	Glu	Phe	Val	Lys	145	150	155	160

Ile Lys Asp Lys Asn Glu Ile Leu Lys Arg Asn Leu Glu Asn Thr Gln  
 165 170 175  
 Asn Gln Ile Lys Ala Glu Tyr Ile Ser Leu Ala Glu His Glu Ala Lys  
 180 185 190  
 Met Ser Ser Leu Ser Gln Ser Met Arg Lys Val Gln Asp Ser Asn Ala  
 195 200 205  
 Glu Ile Leu Ala Asn Tyr Arg Lys Gly Gln Glu Glu Ile Val Thr Leu  
 210 215 220  
 His Ala Glu Ile Lys Ala Gln Lys Lys Glu Leu Asp Thr Ile Gln Glu  
 225 230 235 240  
 Cys Ile Lys Val Lys Tyr Ala Pro Ile Val Ser Phe Glu Glu Cys Glu  
 245 250 255  
 Arg Lys Phe Lys Ala Thr Glu Lys Glu Leu Lys Asp Gln Leu Ser Glu  
 260 265 270  
 Gln Thr Gln Lys Tyr Ser Val Ser Glu Glu Glu Val Lys Lys Asn Lys  
 275 280 285  
 Gln Glu Asn Asp Lys Leu Lys Lys Glu Ile Phe Thr Leu Gln Lys Asp  
 290 295 300  
 Leu Arg Asp Lys Thr Val Leu Ile Glu Lys Ser His Glu Met Glu Arg  
 305 310 315 320  
 Ala Leu Ser Arg Lys Thr Asp Glu Leu Asn Lys Gln Leu Lys Asp Leu  
 325 330 335  
 Ser Gln Lys Tyr Thr Glu Val Lys Asn Val Lys Glu Lys Leu Val Glu  
 340 345 350  
 Glu Asn Ala Lys Gln Thr Ser Glu Ile Leu Ala Val Gln Asn Leu Leu  
 355 360 365  
 Gln Lys Gln His Val Pro Leu Glu Gln Val Glu Ala Leu Lys Lys Ser  
 370 375 380  
 Leu Asn Gly Thr Ile Glu Asn Leu Lys Glu Glu Leu Lys Ser Met Gln  
 385 390 395 400  
 Arg Cys Tyr Glu Lys Glu Gln Gln Thr Val Thr Lys Leu His Gln Leu  
 405 410 415  
 Leu Glu Asn Gln Lys Asn Ser Ser Val Pro Leu Ala Glu His Leu Gln  
 420 425 430  
 Ile Lys Glu Ala Phe Glu Lys Glu Val Gly Ile Ile Lys Ala Ser Leu  
 435 440 445  
 Arg Glu Lys Glu Glu Glu Ser Gln Asn Lys Met Glu Glu Val Ser Lys  
 450 455 460

Leu	Gln	Ser	Glu	Val	Gln	Asn	Thr	Lys	Gln	Ala	Leu	Lys	Lys	Leu	Glu	465	470	475	480
Thr	Arg	Glu	Val	Val	Asp	Leu	Ser	Lys	Tyr	Lys	Ala	Thr	Lys	Ser	Asp	485	490		495
Leu	Glu	Thr	Gln	Ile	Ser	Ser	Leu	Asn	Glu	Lys	Leu	Ala	Asn	Leu	Asn	500	505		510
Arg	Lys	Tyr	Glu	Glu	Val	Cys	Glu	Glu	Val	Leu	His	Ala	Lys	Lys	Lys	515	520		525
Glu	Ile	Ser	Ala	Lys	Asp	Glu	Lys	Glu	Leu	Leu	His	Phe	Ser	Ile	Glu	530	535		540
Gln	Glu	Ile	Lys	Asp	Gln	Lys	Glu	Arg	Cys	Asp	Lys	Ser	Leu	Thr	Thr	545	550		555
Ile	Thr	Glu	Leu	Gln	Arg	Arg	Ile	Gln	Glu	Ser	Ala	Lys	Gln	Ile	Glu	565	570		575
Ala	Lys	Asp	Asn	Lys	Ile	Thr	Glu	Leu	Leu	Asn	Asp	Val	Glu	Arg	Leu	580	585		590
Lys	Gln	Ala	Leu	Asn	Gly	Leu	Ser	Gln	Leu	Thr	Tyr	Thr	Ser	Gly	Asn	595	600		605
Pro	Thr	Lys	Arg	Gln	Ser	Gln	Leu	Ile	Asp	Thr	Leu	Gln	His	Gln	Val	610	615		620
Lys	Ser	Leu	Glu	Gln	Gln	Leu	Ala	Asp	Ala	Asp	Arg	Gln	His	Gln	Glu	625	630		635
Val	Ile	Ala	Ile	Tyr	Arg	Thr	His	Leu	Leu	Ser	Ala	Ala	Gln	Gly	His	645	650		655
Met	Asp	Glu	Asp	Val	Gln	Glu	Ala	Leu	Leu	Gln	Ile	Ile	Gln	Met	Arg	660	665		670
Gln	Gly	Leu	Val	Cys												675			

(2) INFORMATION FOR SEQ ID NO:169:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2041 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

TCTCCCCCT CCCGACACA CACTCACAGG CCGGCATTG ATGGTAATGT ATGCGAGGAA

60

ACAGCAGAGA CTCAGTGATG GCTGTCACGA CCGGAGGGGG GACTCGCAGC CTTACCAGGC	120
ACTTAAGTAT TCATCGAAGA GTCACCCAG TAGCGGTGAT CACAGACATG AAAAGATGCG	180
AGACGCCGGA GATCCTTCAC CACCAAATAA AATGTTGCGG AGATCTGATA GTCCTGAAAA	240
CAAATACAGT GACAGCACAG GTCACAGTAA GGCCAAAAAT GTGCATACTC ACAGAGTTAG	300
AGAGAGGGAT GGTGGGACCA GTTACTCTCC ACAAGAAAAT TCACACAACC ACAGTGCTCT	360
TCATAGTTCA AATTCACATT CTTCTAATCC AAGCAATAAC CCAAGCAAAA CTTCAGATGC	420
ACCTTATGAT TCTGCAGATG ACTGGTCTGA GCATATTAGC TCTTCTGGGA AAAAGTACTA	480
CTACAATTGT CGAACAGAAG TTTCACAATG GGAAAAACCA AAAGAGTGGC TTGAAAGAGA	540
ACAGAGACAA AAAGAAGCAA ACAAGATGGC AGTCAACAGC TTCCCAAAAG ATAGGGATTA	600
CAGAAGAGAG GTGATGCAAG CAACAGCCAC TAGTGGGTTT GCCAGTGGAA AATCTACATC	660
AGGAGACAAA CCCGTATCAC ATTCTTGCAC AACTCCTTCC ACGTCTTCTG CCTCTGGACT	720
GAACCCACCA TCTGCACCTC CAACATCTGC TTCAGCGGTC CCTGTTTCTC CTGTTCCACA	780
GTCGCCAATA CCTCCCTTAC TTCAGGACCC AAATCTTCTT AGACAATTGC TTCCTGCTTT	840
GCAAGCCACG CTGCAGCTTA ATAATTCTAA TGTGGACATA TCTAAAATAA ATGAAGTTCT	900
TACAGCAGCT GTGACACAAG CCTCACTGCA GTCTATAATT CATAAGTTTC TTAGTGCTGG	960
ACCATCTGCT TTCAACATAA CGTCTCTGAT TTCTCAAGCT GCTCAGCTCT CTACACAAGC	1020
CCAGCCATCT AATCAGTCTC CGATGTCTTT AACATCTGAT GCGTCATCCC CAAGATCATA	1080
TGTTTCTCCA AGAATAAGCA CACCTCAAAC TAACACAGTC CCTATCAAAC CTTTGATCAG	1140
TACTCCTCCT GTTTCATCAC AGCCAAAGGT TAGTACTCCA GTAGTTAAGC AAGGACCAGT	1200
GTCACAGTCA GCCACACAGC AGCCTGTAAC TGCTGACAAG CAGCAAGGTC ATGAACCTGT	1260
CTCTCCTCGA AGTCTTCAGC GCTCAAGCCA GAGAAGTCCA TCACCTGGTC CCAATCATAC	1320
TTCTAATAGT AGTAATGCAT CAAATGCAAC AGTTGTACCA CAGAATTCTT CTGCCCCGATC	1380
CACGTGTTCA TTAACGCCTG CACTAGCAGC ACACTTCAGT GAAAATCTCA TAAACACGT	1440
TCAAGGATGG CCTGCAGATC ATGCAGAGAA GCAGGCATCA AGATTACGCG AAGAAGCGCA	1500
TAACATGGGA ACTATTCACA TGTCCGAAAT TTGTACTGAA TTAAAAAATT TAAGATCTTT	1560
AGTCCGAGTA TGTGAAATTC AAGCAACTTT GCGAGAGCAA AGGATACTAT TTTTGAGACA	1620
ACAAATTAAG GAACTTGAAA AGCTAAAAAA TCAGAATTCC TTCATGGTGT GAAGATGTGA	1680
ATAATTGCAC ATGGTTTTGA GAACAGGAAC TGTAATCTG TTGCCCAATC TTAACATTTT	1740

TGAGCTGCAT TTAAGTAGAC TTTGGACCGT TAAGCTGGGC AAAGGAAATG ACAAGGGGAC 1800  
 GGGGTCTGTG AGAGTCAATT CAGGGGAAAG ATACAAGATT GATTTGTAAA ACCCTTGAAA 1860  
 TGTAGATTTT TTGTAGATGT ATCCTTCACG TTGTAAATAT GTTTTGTAGA GTGAAGCCAT 1920  
 GGAAGCCAT GTGTAACAGA GCTTAGACAT CCAAACTAA TCAATGCTGA GGTGGCTAAA 1980  
 TACCTAGCCT TTTACATGTA AACCTGTCTG CAAAATTAGC TTTTAAATAA AAAAAAAAAA 2040  
 A 2041

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

Met	Arg	Gly	Asn	Ser	Arg	Asp	Ser	Val	Met	Ala	Val	Thr	Thr	Gly	Gly	1	5	10	15
Gly	Thr	Arg	Ser	Leu	Thr	Arg	His	Leu	Ser	Ile	His	Arg	Arg	Val	Thr	20	25	30	
Pro	Val	Ala	Val	Ile	Thr	Asp	Met	Lys	Arg	Cys	Glu	Thr	Pro	Glu	Ile	35	40	45	
Leu	His	His	Gln	Ile	Lys	Cys	Cys	Gly	Asp	Leu	Ile	Val	Leu	Lys	Thr	50	55	60	
Asn	Thr	Val	Thr	Ala	Gln	Val	Thr	Val	Arg	Pro	Lys	Met	Cys	Ile	Leu	65	70	75	80
Thr	Glu	Leu	Glu	Arg	Gly	Met	Val	Gly	Pro	Val	Thr	Leu	His	Lys	Lys	85	90	95	
Ile	His	Thr	Thr	Thr	Val	Leu	Phe	Ile	Val	Gln	Ile	His	Ile	Leu	Leu	100	105	110	
Ile	Gln	Ala	Ile	Thr	Gln	Ala	Lys	Leu	Gln	Met	His	Leu	Met	Ile	Leu	115	120	125	
Gln	Met	Thr	Gly	Leu	Ser	Ile	Leu	Ala	Leu	Leu	Gly	Lys	Ser	Thr	Thr	130	135	140	
Thr	Ile	Val	Glu	Gln	Lys	Phe	His	Asn	Gly	Lys	Asn	Gln	Lys	Ser	Gly	145	150	155	160
Leu	Lys	Glu	Asn	Arg	Asp	Lys	Lys	Lys	Gln	Thr	Arg	Trp	Gln	Ser	Thr				

165

170

175

Ala Ser Gln Lys Ile Gly Ile Thr Glu Glu Arg  
180 185

## (2) INFORMATION FOR SEQ ID NO:171:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1163 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

GCCCTATCCA CTTAATAGAT GCCAATTCAA AGAGGTTAAA TGATTAGACT AAGGCACCTA 60  
ACTTATGTGA GTGTCAGGCT TCAATGCCTG TGTTAGAGCT ACTCCTTCAC ACAAATAGT 120  
TCAGAACATA GAGAAGGACC AAGGTTAATA AATGATTTTC ATCCCAAACA CTAAACATGA 180  
TTGATGGGTA GAGGCTGCCC GAAGTACTGT GTAAAGATGG AATCTGAGAT AGAAGAATGC 240  
TGTGGTCAAT TAGTAATTCT TGCCCATGGA GGGATTAGTG ACACATGCCT TGTATATTTG 300  
TCATCTGTGG CCTAAACTCT GCCCCTGAAG GTTTGTTTTT TAATTCAGAG GTTTAAATTA 360  
ATCTAGCCCA CTTAATAAAA CCAGAGATCC TATGGGAAAT TTAGCCTAAG ACAGTGCTGG 420  
AAATTGCCAT ATGTTGATAC AAAGAAGTGT TTGGCCACAT TACAGGTCTC AGACTCAACT 480  
GCTATGTGTG ACTGCCGCTC TGTGCCTATG TCTTGCTTTT TTGCTGAGTT CCCTATTTCC 540  
ATATCTCCAG GTGAATCCAT GAGAAGCGAG AGGGTGGCTG AGAGGCCTGG GCCTCTGGGA 600  
TTCCACCTTG CTATCTCTGC TCTTCAACCA TTGTTTTAGA CTCTGAACAC CAGATCCTCA 660  
TATCTGAAAG TGATTTGGAG ACCTGGGCAT CAAGTGCTCT TTTAAGAAGG GGCTATCCCA 720  
GAGGACTGTT CAAAAGTCTC ATTCAATAGA GATGTTGGAG TCCAGAACA AAGTTAGGGA 780  
GCAAACCAGT AACCTATGCT GGTSGTAACA GAGGATCCTA CAATTACGTT TGTTTTTAAG 840  
ACAGGATTTT GCTGTGTTGC CCAGACTGGT CTCAAACCTC TGGGTTCAAG AGATCCATCC 900  
TCCACCTCA GTCTCCTGAA AGCTGGGATG ACAGGCACAT GCCACCACAC CTAGCTCCTT 960  
ACAACCATTT ATTTTAACTT ATTTCAATTA TAACTGGTAT CTTTCATTTG TATGTGGCAG 1020  
CTAGAGATTT ATATAGGATG GAAGTAATTT ATTTTAAATT TAAATATTTT ATGTTGAACT 1080  
GTTTGCCTTG TATGGAACAT TTTACTTGGC CAATTCAAAT AAAAATAAAG TCAGCTTTGT 1140

## (2) INFORMATION FOR SEQ ID NO:172:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 43 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

Met	Leu	Ile	Gln	Arg	Ser	Val	Trp	Pro	His	Tyr	Arg	Ser	Gln	Thr	Gln
1				5				10					15		
Leu	Leu	Cys	Val	Thr	Ala	Ala	Leu	Cys	Leu	Cys	Leu	Ala	Phe	Leu	Leu
			20				25					30			
Ser	Ser	Leu	Phe	Pro	Tyr	Leu	Gln	Val	Asn	Pro					
		35				40									

## (2) INFORMATION FOR SEQ ID NO:173:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 3067 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

GCGGTGGCTG	AGGCGGCTGG	GCCTAGGGTG	CAGCGGGCGC	GTCTGCGGCT	GGTGTGGCG	60
CATCTCTAGA	TCCTTTCCCG	GAGTTCAGTT	ATGGGTGTGA	GAGGTTTGCA	AGGATTTGTG	120
GGAAGTACCT	GCCCACATAT	ATGTACAGTA	GTAAATTTCA	AAGAACTGGC	AGAGCACCAC	180
CGAAGCAAGT	ATCCTGGATG	TACCCCTACC	ATTGTGGTTG	ATGCCATGTG	TTGTCTCAGA	240
TATTGGTATA	CTCCAGAATC	TTGGATCTGC	GGTGGCCAGT	GGCGAGAATA	CTTTTCTGCT	300
TTGCGAGATT	TTGTTAAAAC	TTTTACGGCA	GCTGGGATCA	AGTTGATATT	CTTCTTTGAT	360
GGCATGGTGG	AGCAGGATAA	GAGAGATGAA	TGGGTGAAAC	GAAGGCTCAA	GAACAACAGG	420
GAGATATCCA	GGATTTTTC	TTACATCAAG	TCACACAAGG	AGCAGCCAGG	CAGAAATATG	480
TTCTTCATCC	CCTCAGGGCT	AGCTGTGTTT	ACACGATTTG	CTCTAAAGAC	ACTGGGCCAG	540
GAACTTTGT	GTTCTTTGCA	GGAAGCAGAT	TATGAGGTAG	CTTCCTATGG	CCTCCAGCAT	600



AACTGTCTTG	GGATTCTGGG	GGAAGACACT	GATTACCTAA	TCTATGACAC	TTGTCCCTAC	660
TTTTCAATTA	GCGAGCTCTG	CCTAGAGAGC	CTGGACACCG	TCATGCTCTG	CAGAGAGAAG	720
CTCTGTGAGA	GTCTGGGCCT	CTGTGTGGCC	GACCTTCCTC	TTCTGGCCTG	CCTCCTTGGC	780
GACGACATAA	TCCCAGAGGG	CATGTTTGAA	AGCTTTAGGT	ACAAATGCTT	ATCGTCCTAC	840
ACCTCTGTAA	AAGAGAACTT	TGACAAAAAA	GGTAACATCA	TATTAGCTGT	GTCAGACCAT	900
ATATCGAAAG	TTCTTTACTT	GTATCAAGGT	GAGAAAAAAT	TAGAAGAGAT	ATTACCTCTG	960
GGACCAAACA	AAGCTCTTTT	TTATAAAGGA	ATGGCATCAT	ATCTTTTACC	AGGACAAAAA	1020
TCTCCATGGT	TTTTCAAAA	ACCCAAAGGT	GTAATAACTT	TGGACAAACA	AGTAATATCC	1080
ACGAGTTCAG	ACGCCGAATC	CAGGGAAGAA	GTTCCCATGT	G TTCAGATGC	TGAATCCAGG	1140
CAAGAAGTTC	CCATGTGTAC	AGGCCCTGAA	TCCAGGCGAG	AAGTTCCCGT	GTATACAGAT	1200
TCTGAACCCA	GGCAAGAAGT	TCCCATGTGT	TCAGACCCTG	AACCCAGGCA	AGAAGTTCCC	1260
ACATGTACAG	GCCCTGAATC	CAGGCGAGAA	GTTCCCATGT	G TTCAGACCC	TGAACCCAGG	1320
CAAGAAGTTC	CCATGTGTAC	AGGCCCTGAA	GCCAGGCAAG	AAGTTCCCAT	GTATACAGAC	1380
TCTGAACCCA	GGCAAGAAGT	TCCCATGTAT	ACAGACTCTG	AACCCAGGCA	AGAAGTTCCC	1440
ATGTATACAG	GCTCTGAACC	CAGGCAAGAA	GTTCCCATGT	ATACAGGCCC	TGAATCCAGG	1500
CAAGAAGTTC	CCATGTATAC	AGGCCCTGAA	TCCAGGCAAG	AAGTTTTAAT	ACGGACAGAC	1560
CCTGAATCTA	GGCAAGAAAT	TATGTGTACA	GGCCATGAAT	CCAAACAGGA	AGTTCCCAT	1620
TGTACAGATC	CTATATCCAA	GCAAGAAGAC	TCCATGTGTA	CACACGCTGA	AATCAATCAA	1680
AAATTACCTG	TAGCAACAGA	TTTTGAATTT	AAGCTAGAAG	CTCTCATGTG	TACAAACCCT	1740
GAAATTAAAC	AAGAAGACCC	CACAAATGTG	GGGCCTGAAG	TAAAGCAACA	AGTAACCATG	1800
GTTTCAGACA	CTGAAATCTT	AAAGGTTGCT	AGAACACATC	ACGTCCAAGC	AGAAAGCTAC	1860
CTGGTGTACA	ACATCATGAG	CAGTGGAGAG	ATTGAATGCA	GCAACACCCT	AGAAGATGAG	1920
CTTGACCAGG	CCTTACCCAG	CCAGGCCTTC	ATTTACCGTC	CCATTGACA	GCGGGTCTAC	1980
TCACTCTTAC	TGGAGGACTG	TCAAGATGTC	ACCAGCACCT	GCCTAGCTGT	CAAGGAGTGG	2040
TTTGTGTATC	CTGGGAACCC	ACTGAGGCAC	CCGACCTCG	TCAGGCCGCT	GCAGATGACC	2100
ATTCCAGGGG	GAACGCCTAG	TTTGAAAATA	TTATGGCTGA	ACCAAGAGCC	AGAAATACAG	2160
GTTGCGCGCT	TGGACACACT	CCTAGCCTGT	TTCAATCTTT	CCTCCTCAAG	AGAAGAGCTG	2220
CAGGCTGTCTG	AAAGCCCATT	TCAAGCTTTG	TGCTGCCTCT	TGATCTACCT	CTTTGTCCAG	2280

GTGGACACGC TTTGCCTGGA GGATTTGCAT GCGTTTATTG CGCAGGCCTT GTGCCTCCAA 2340  
GGAAAATCCA CCTCGCAGCT TGTAATCTA CAGCCTGATT ACATCAACCC CAGAGCCGTG 2400  
CAGCTGGGCT CCCTTCTCGT CCGCGGCCTC ACCACTCTGG TTTTAGTCAA CAGCGCATGT 2460  
GGCTTCCCTT GGAAGACGAG TGATTTTCATG CCCTGGAATG TATTTGACGG GAAGCTTTTT 2520  
CATCAGAAGT ACTTGCAATC TGAAAAGGGT TATGCTGTGG AGGTTCTTTT AGAACAAAAT 2580  
GGAGGTGGGG AAGACAGGGC TCCAGCTACC ACAGGACGGG CTCTGGGTAT AGCCGTTCCA 2640  
GTCAGGGACA GCCGTGGAGA GACCAGGGAC CAGGAAGCAG ACAGTATGAG CATGACCAGT 2700  
GGAGAAGGTA CTAGTCAACC TCCAGAAAGA GTATGGAGAG AAAAAGAGGC ACACCTGGAC 2760  
GCAGAGCCCT GCCAGCGCCC TCCTCTGCTG TTGCAGCTGC AAGGAGACCA TGCCTGTGGG 2820  
AGCCAGGCCT CGCTTGCATG AAGAAGGAAC GATGCCTTTT TCAATGGTGT CTCCCTCCCA 2880  
TTGTGCAGAA GAGCTTTTGT TGGCTTCTCT CCCGAGCTTG TGCCTGATTC TGTGGCCCAA 2940  
AACAAATCATT GTTAACATCT TCATGTGTTT CATTCTGATC TTTCATTCAT ATATATGATG 3000  
CCTAGCTAAT TTCATTTTAA AATAAATGGG AATCTGTTGT AAAAAAAAAA AAAAAAAAAA 3060  
AAAAAAA 3067

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 916 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

Met	Gly	Val	Arg	Gly	Leu	Gln	Gly	Phe	Val	Gly	Ser	Thr	Cys	Pro	His
1				5				10					15		
Ile	Cys	Thr	Val	Val	Asn	Phe	Lys	Glu	Leu	Ala	Glu	His	His	Arg	Ser
			20					25					30		
Lys	Tyr	Pro	Gly	Cys	Thr	Pro	Thr	Ile	Val	Val	Asp	Ala	Met	Cys	Cys
			35					40					45		
Leu	Arg	Tyr	Trp	Tyr	Thr	Pro	Glu	Ser	Trp	Ile	Cys	Gly	Gly	Gln	Trp
			50				55				60				
Arg	Glu	Tyr	Phe	Ser	Ala	Leu	Arg	Asp	Phe	Val	Lys	Thr	Phe	Thr	Ala
						70				75					80

Ala	Gly	Ile	Lys	Leu	Ile	Phe	Phe	Phe	Asp	Gly	Met	Val	Glu	Gln	Asp	
				85					90						95	
Lys	Arg	Asp	Glu	Trp	Val	Lys	Arg	Arg	Leu	Lys	Asn	Asn	Arg	Glu	Ile	
			100					105						110		
Ser	Arg	Ile	Phe	His	Tyr	Ile	Lys	Ser	His	Lys	Glu	Gln	Pro	Gly	Arg	
		115					120					125				
Asn	Met	Phe	Phe	Ile	Pro	Ser	Gly	Leu	Ala	Val	Phe	Thr	Arg	Phe	Ala	
	130					135					140					
Leu	Lys	Thr	Leu	Gly	Gln	Glu	Thr	Leu	Cys	Ser	Leu	Gln	Glu	Ala	Asp	
145					150					155					160	
Tyr	Glu	Val	Ala	Ser	Tyr	Gly	Leu	Gln	His	Asn	Cys	Leu	Gly	Ile	Leu	
				165					170					175		
Gly	Glu	Asp	Thr	Asp	Tyr	Leu	Ile	Tyr	Asp	Thr	Cys	Pro	Tyr	Phe	Ser	
			180					185						190		
Ile	Ser	Glu	Leu	Cys	Leu	Glu	Ser	Leu	Asp	Thr	Val	Met	Leu	Cys	Arg	
		195					200					205				
Glu	Lys	Leu	Cys	Glu	Ser	Leu	Gly	Leu	Cys	Val	Ala	Asp	Leu	Pro	Leu	
	210					215					220					
Leu	Ala	Cys	Leu	Leu	Gly	Asp	Asp	Ile	Ile	Pro	Glu	Gly	Met	Phe	Glu	
225					230					235					240	
Ser	Phe	Arg	Tyr	Lys	Cys	Leu	Ser	Ser	Tyr	Thr	Ser	Val	Lys	Glu	Asn	
				245					250					255		
Phe	Asp	Lys	Lys	Gly	Asn	Ile	Ile	Leu	Ala	Val	Ser	Asp	His	Ile	Ser	
			260					265					270			
Lys	Val	Leu	Tyr	Leu	Tyr	Gln	Gly	Glu	Lys	Lys	Leu	Glu	Glu	Ile	Leu	
		275					280					285				
Pro	Leu	Gly	Pro	Asn	Lys	Ala	Leu	Phe	Tyr	Lys	Gly	Met	Ala	Ser	Tyr	
	290					295					300					
Leu	Leu	Pro	Gly	Gln	Lys	Ser	Pro	Trp	Phe	Phe	Gln	Lys	Pro	Lys	Gly	
305					310					315					320	
Val	Ile	Thr	Leu	Asp	Lys	Gln	Val	Ile	Ser	Thr	Ser	Ser	Asp	Ala	Glu	
				325					330					335		
Ser	Arg	Glu	Glu	Val	Pro	Met	Cys	Ser	Asp	Ala	Glu	Ser	Arg	Gln	Glu	
			340					345					350			
Val	Pro	Met	Cys	Thr	Gly	Pro	Glu	Ser	Arg	Arg	Glu	Val	Pro	Val	Tyr	
		355					360					365				
Thr	Asp	Ser	Glu	Pro	Arg	Gln	Glu	Val	Pro	Met	Cys	Ser	Asp	Pro	Glu	
	370					375					380					

Pro	Arg	Gln	Glu	Val	Pro	Thr	Cys	Thr	Gly	Pro	Glu	Ser	Arg	Arg	Glu	
385					390					395					400	
Val	Pro	Met	Cys	Ser	Asp	Pro	Glu	Pro	Arg	Gln	Glu	Val	Pro	Met	Cys	
				405					410					415		
Thr	Gly	Pro	Glu	Ala	Arg	Gln	Glu	Val	Pro	Met	Tyr	Thr	Asp	Ser	Glu	
			420					425					430			
Pro	Arg	Gln	Glu	Val	Pro	Met	Tyr	Thr	Asp	Ser	Glu	Pro	Arg	Gln	Glu	
		435					440					445				
Val	Pro	Met	Tyr	Thr	Gly	Ser	Glu	Pro	Arg	Gln	Glu	Val	Pro	Met	Tyr	
	450					455					460					
Thr	Gly	Pro	Glu	Ser	Arg	Gln	Glu	Val	Pro	Met	Tyr	Thr	Gly	Pro	Glu	
465					470					475					480	
Ser	Arg	Gln	Glu	Val	Leu	Ile	Arg	Thr	Asp	Pro	Glu	Ser	Arg	Gln	Glu	
				485					490					495		
Ile	Met	Cys	Thr	Gly	His	Glu	Ser	Lys	Gln	Glu	Val	Pro	Ile	Cys	Thr	
			500					505					510			
Asp	Pro	Ile	Ser	Lys	Gln	Glu	Asp	Ser	Met	Cys	Thr	His	Ala	Glu	Ile	
		515					520					525				
Asn	Gln	Lys	Leu	Pro	Val	Ala	Thr	Asp	Phe	Glu	Phe	Lys	Leu	Glu	Ala	
	530					535					540					
Leu	Met	Cys	Thr	Asn	Pro	Glu	Ile	Lys	Gln	Glu	Asp	Pro	Thr	Asn	Val	
545					550					555					560	
Gly	Pro	Glu	Val	Lys	Gln	Gln	Val	Thr	Met	Val	Ser	Asp	Thr	Glu	Ile	
				565					570					575		
Leu	Lys	Val	Ala	Arg	Thr	His	His	Val	Gln	Ala	Glu	Ser	Tyr	Leu	Val	
			580					585					590			
Tyr	Asn	Ile	Met	Ser	Ser	Gly	Glu	Ile	Glu	Cys	Ser	Asn	Thr	Leu	Glu	
		595					600					605				
Asp	Glu	Leu	Asp	Gln	Ala	Leu	Pro	Ser	Gln	Ala	Phe	Ile	Tyr	Arg	Pro	
	610					615					620					
Ile	Arg	Gln	Arg	Val	Tyr	Ser	Leu	Leu	Leu	Glu	Asp	Cys	Gln	Asp	Val	
625					630					635					640	
Thr	Ser	Thr	Cys	Leu	Ala	Val	Lys	Glu	Trp	Phe	Val	Tyr	Pro	Gly	Asn	
				645					650					655		
Pro	Leu	Arg	His	Pro	Asp	Leu	Val	Arg	Pro	Leu	Gln	Met	Thr	Ile	Pro	
			660					665					670			
Gly	Gly	Thr	Pro	Ser	Leu	Lys	Ile	Leu	Trp	Leu	Asn	Gln	Glu	Pro	Glu	
		675					680					685				

Ile	Gln	Val	Arg	Arg	Leu	Asp	Thr	Leu	Leu	Ala	Cys	Phe	Asn	Leu	Ser	690	695	700
Ser	Ser	Arg	Glu	Glu	Leu	Gln	Ala	Val	Glu	Ser	Pro	Phe	Gln	Ala	Leu	705	710	715
Cys	Cys	Leu	Leu	Ile	Tyr	Leu	Phe	Val	Gln	Val	Asp	Thr	Leu	Cys	Leu	725	730	735
Glu	Asp	Leu	His	Ala	Phe	Ile	Ala	Gln	Ala	Leu	Cys	Leu	Gln	Gly	Lys	740	745	750
Ser	Thr	Ser	Gln	Leu	Val	Asn	Leu	Gln	Pro	Asp	Tyr	Ile	Asn	Pro	Arg	755	760	765
Ala	Val	Gln	Leu	Gly	Ser	Leu	Leu	Val	Arg	Gly	Leu	Thr	Thr	Leu	Val	770	775	780
Leu	Val	Asn	Ser	Ala	Cys	Gly	Phe	Pro	Trp	Lys	Thr	Ser	Asp	Phe	Met	785	790	795
Pro	Trp	Asn	Val	Phe	Asp	Gly	Lys	Leu	Phe	His	Gln	Lys	Tyr	Leu	Gln	805	810	815
Ser	Glu	Lys	Gly	Tyr	Ala	Val	Glu	Val	Leu	Leu	Glu	Gln	Asn	Gly	Gly	820	825	830
Gly	Glu	Asp	Arg	Ala	Pro	Ala	Thr	Thr	Gly	Arg	Ala	Leu	Gly	Ile	Ala	835	840	845
Val	Pro	Val	Arg	Asp	Ser	Arg	Gly	Glu	Thr	Arg	Asp	Gln	Glu	Ala	Asp	850	855	860
Ser	Met	Ser	Met	Thr	Ser	Gly	Glu	Gly	Thr	Ser	Gln	Pro	Pro	Glu	Arg	865	870	875
Val	Trp	Arg	Glu	Lys	Glu	Ala	His	Leu	Asp	Ala	Glu	Pro	Cys	Gln	Arg	885	890	895
Pro	Pro	Leu	Leu	Leu	Gln	Leu	Gln	Gly	Asp	His	Ala	Cys	Gly	Ser	Gln	900	905	910
Ala	Ser	Leu	Ala													915		

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1914 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

AGCTGTCTGC TCTCCTGGCA GGAATCGCTG AGGGAGGGAA ACGCGGCTCT GAATCAGCCC	60
AGAACGAGCC TTCGGAAGC TCACCCTCCG ATCTCGGTGT GATTGTTGTG ATTGTTGTGA	120
TTTCCTGTCT CGTTTGCCTT GACCGCCATG TGAAAGAATC TGTTCCCCAG CTAGGTGGGG	180
AAAATTCACA GGTGGGCTGT CTGTAGAGAG AACTGGCTGA TTAAAGGCTT CTCGTCCCGA	240
TTTTGTGATA GCCAAGTGCT TGGCCTGGTC GACGGTCTTT GCTCCTTTAC AAATAAAGTG	300
TTCTGTTTCA GTTCGTCCCA AGTTTTCCAT GAAGGGCAGT GGTTCCCTGA CCTCCCAGGT	360
GCCTGGGCTT CCCAGGTTT CTGATCTGGG GCTTGGGGCC CTGTGTTTGG GGATCGTGGC	420
ACTGTGTGCA CCAGCCTGGA AGCACTGGGC CAGTCTTGGC CAAGCTTTCC ATCAGGGATG	480
ATTTGATCTT GGTGCTACAG GTCTGTGGTA CGACCATTGT TCCACACCAC ATGTCATTAA	540
TAATGCTTCC CATGCTTCTG CTTGCAAATG ACCAGCCTTC CAAACAGCCA GAGCTGTTTC	600
GAGGTGTTTC TGCAGGCAGG TGCAGGCGTG CCCTCAAATA AGCTTTGCCA ATGGAGTCTC	660
AGCAAGAGCA AAACCTGGTC AGGAAAGACA AAGCCTGGGA ATCCACCCCC ATGCCCTGCA	720
GGTTGGCTGG CCCTGGAGCC ATTTATTATA GTGCTAATCA TGTTTCTAGG CAGGTGCAGA	780
TGGCAAGGGC AGTGTCTTGG TGAGCTTTTT AGCACGAAGA GCCAGGTCTG TCGAAGCCTT	840
TGTGAGAGCT GGAAACGCAG GTGTGCTGGG CATGCGCAGT ATGGGGTTTC GGGCTCAGGG	900
CTTGCCCTTT GGCATCAGAC AGACCTGGCT TCGCATCCTG GATTTGCTTC TGACGTGCAC	960
CCTTCCCTTT GGGTCTCGTG ATGTGAAATG GAGATGTTGT CATTTGTGAG GGCTCCATGA	1020
AGTTTCGTTG AAATGACAAA TACTAATTTT TTCATCTGTG AAATGGAGAT AATAGTGCTG	1080
ACCTCAGAAC AGCTGAGAGG ACTAAATGAA ATGATGTTGG ATGTAGCCAT AAAGAACGAA	1140
GTCAGGCACT GGTGCACGCC TGGAATCCCA GCTCTTGGA GACCGAGACA GGTGGATTGC	1200
TTGAGCTCAG GAGTTTGAGA CCAGCCTGAG CAACATAGGG AGGTCCAGTC TCTACAAAAA	1260
ATATGAAAAG TAGCTGGGCG TGGTGGCGCA TGCCTGTAGT CCCACTACTT GGAAGGCTTC	1320
GTTGGGAGGA TCACTTGAGC CCAGAAGATT GAGGCTGCAG TAAGCCGTGA TCGTGCCACT	1380
GCATTCCAGC CTGGGCAACA GAGCGAGACA CTGTCTCAA TAAAAAAGAT GGGAATAGTA	1440
GAACTGGGG GCTCCAGAAG GAGGGAGGGA GGGAGGAAGG GGAGGAAGGG CTGAAATGCT	1500
TTCTATTGGA TACTATCTGG GCATATTACT TCCTGTGGTT CACTGTCTGG GTGACAGGAT	1560
TCATAGAAGC CCAAACCTTA GCACCACGCA GCATACCCTT GTAACAAAGC CGCACACGTA	1620
CGCCCTCAAG CTAAAACAAA AGTGGACCGG GAGGCCGAGG TCGGGGGATC ATGAGGTCAG	1680

GAGTTTGAGA CCAGCCTGGC AGATAACGGT GAAACCCCGT CTCTACTAAA AATACCAAAA 1740  
AAAGTTAGCC GGACATGGTG GCAGGTGCCT GTAGTCCCAG CTACTTGGGA GGCTGGGGCA 1800  
GAAGAATCGC TTGAACCCAG GAGGCGGAGG TTGCAGTGAG CCGAGATTGC GCCACTGCAC 1860  
TCCAGCCTGT GCGACAGAGT GAGACTCCGT CTCAAAAAAA AAAAAAAAAA AAAA 1914

(2) INFORMATION FOR SEQ ID NO:176:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 137 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

Met	Thr	Ser	Leu	Pro	Asn	Ser	Gln	Ser	Cys	Phe	Glu	Val	Phe	Leu	Gln	1	5	10	15
Ala	Gly	Ala	Gly	Val	Pro	Ser	Asn	Lys	Leu	Cys	Gln	Trp	Ser	Leu	Ser	20	25	30	
Lys	Ser	Lys	Thr	Trp	Ser	Gly	Lys	Thr	Lys	Pro	Gly	Asn	Pro	Pro	Pro	35	40	45	
Cys	Pro	Ala	Gly	Trp	Leu	Ala	Leu	Glu	Pro	Phe	Ile	Ile	Val	Leu	Ile	50	55	60	
Met	Phe	Leu	Gly	Arg	Cys	Arg	Trp	Gln	Gly	Gln	Cys	Leu	Gly	Glu	Leu	65	70	75	80
Phe	Ser	Thr	Lys	Ser	Gln	Val	Cys	Arg	Ser	Leu	Cys	Glu	Ser	Trp	Lys	85	90	95	
Arg	Arg	Cys	Ala	Gly	His	Ala	Gln	Tyr	Gly	Val	Ser	Gly	Ser	Gly	Leu	100	105	110	
Ala	Leu	Trp	His	Gln	Thr	Asp	Leu	Ala	Ser	His	Pro	Gly	Phe	Ala	Ser	115	120	125	
Asp	Val	His	Pro	Ser	Leu	Trp	Val	Ser	130	135									

(2) INFORMATION FOR SEQ ID NO:177:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 575 base pairs  
(B) TYPE: nucleic acid

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

```
CCGACTCCCT TCTTTATGGC GTCGCTCCTG TGCTGTGGGC CGAAGCTGGC CGCCTGCGGC      60
ATCGTCCTCA GCGCCTGGGG AGTGATCATG TTGATAATGC TCGGAATATT TTTCAATGTC      120
CATTCCGCTG TGTTGATTGA GGACGTTCCC TTCACGGAGA AAGATTTTGA GAATGGCCCC      180
CAGAACATAT ACAACCTTTA CGAGCAAGTC AGCTACAAC TTTTCATCGC TGCAGGCCTT      240
TACCTCCTCC TCGGAGGCTT CTCTTTCTGC CAAGTTCGGC TCAATAAGCG CAAGGAATAC      300
ATGGTGCGCT AGGGCCCCGG CGCGTTTCCC CGCTCCAGCC CCTCCTCTAT TTAAAGACTC      360
CCTGCACCGT GTCACCCAGG TCGCGTCCCA CCCTTGCCGG CGCCCTCTGT GGGACTGGGT      420
TTCCCGGGCG AGAGACTGAA TCCCTTCTCC CATCTCTGGC ATCCGGCCCC CGTGGAGAGG      480
GCTGAGGCTG GGGGGCTGTT CCGTCTCTCC ACCCTTCGCT GTGTCCCGTA TCTCAATAAA      540
GAGAATCTGC TCTCTTCAAA AAAAAAAAAA AAAAAA      575
```

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 98 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

```
Met Ala Ser Leu Leu Cys Cys Gly Pro Lys Leu Ala Ala Cys Gly Ile
1           5           10           15
Val Leu Ser Ala Trp Gly Val Ile Met Leu Ile Met Leu Gly Ile Phe
20          25          30
Phe Asn Val His Ser Ala Val Leu Ile Glu Asp Val Pro Phe Thr Glu
35          40          45
Lys Asp Phe Glu Asn Gly Pro Gln Asn Ile Tyr Asn Leu Tyr Glu Gln
50          55          60
Val Ser Tyr Asn Cys Phe Ile Ala Ala Gly Leu Tyr Leu Leu Leu Gly
65          70          75          80
Gly Phe Ser Phe Cys Gln Val Arg Leu Asn Lys Arg Lys Glu Tyr Met
```



Val Arg

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

GNAGCCCAGGA GTCTTCTCAA CCTCTTCC

29

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

ANCAGTCGCAA GTGCATAGTA ACCCAGTA

29

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

TNCTCAGCTTT TATTTGGTTC TGAGTGTT

29

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

TNTGCTCAGAC CAGTCATCTG CAGAATCA

29

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

TNCAGCACTGT CTTAGGCTAA ATTTCCCA

29

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

GNATTCGGCGT CTGAACTCGT GGATATTA

29

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

ANATGCCCGAGA TAGTATCCAA TAGAAAGC

29

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

CNACAGCACAG GAGCGACGCC ATAAAGAA

29

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 543 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

Met Val Met Tyr Ala Arg Lys Gln Gln Arg Leu Ser Asp Gly Cys His  
1 .5 10 15

Asp Arg Arg Gly Asp Ser Gln Pro Tyr Gln Ala Leu Lys Tyr Ser Ser  
20 25 30

Lys Ser His Pro Ser Ser Gly Asp His Arg His Glu Lys Met Arg Asp  
35 40 45

Ala Gly Asp Pro Ser Pro Pro Asn Lys Met Leu Arg Arg Ser Asp Ser  
50 55 60

Pro Glu Asn Lys Tyr Ser Asp Ser Thr Gly His Ser Lys Ala Lys Asn  
65 70 75 80

Val His Thr His Arg Val Arg Glu Arg Asp Gly Gly Thr Ser Tyr Ser  
85 90 95

Pro Gln Glu Asn Ser His Asn His Ser Ala Leu His Ser Ser Asn Ser  
 100 105 110  
 His Ser Ser Asn Pro Ser Asn Asn Pro Ser Lys Thr Ser Asp Ala Pro  
 115 120 125  
 Tyr Asp Ser Ala Asp Asp Trp Ser Glu His Ile Ser Ser Ser Gly Lys  
 130 135 140  
 Lys Tyr Tyr Tyr Asn Cys Arg Thr Glu Val Ser Gln Trp Glu Lys Pro  
 145 150 155 160  
 Lys Glu Trp Leu Glu Arg Glu Gln Arg Gln Lys Glu Ala Asn Lys Met  
 165 170 175  
 Ala Val Asn Ser Phe Pro Lys Asp Arg Asp Tyr Arg Arg Glu Val Met  
 180 185 190  
 Gln Ala Thr Ala Thr Ser Gly Phe Ala Ser Gly Lys Ser Thr Ser Gly  
 195 200 205  
 Asp Lys Pro Val Ser His Ser Cys Thr Thr Pro Ser Thr Ser Ser Ala  
 210 215 220  
 Ser Gly Leu Asn Pro Thr Ser Ala Pro Pro Thr Ser Ala Ser Ala Val  
 225 230 235 240  
 Pro Val Ser Pro Val Pro Gln Ser Pro Ile Pro Pro Leu Leu Gln Asp  
 245 250 255  
 Pro Asn Leu Leu Arg Gln Leu Leu Pro Ala Leu Gln Ala Thr Leu Gln  
 260 265 270  
 Leu Asn Asn Ser Asn Val Asp Ile Ser Lys Ile Asn Glu Val Leu Thr  
 275 280 285  
 Ala Ala Val Thr Gln Ala Ser Leu Gln Ser Ile Ile His Lys Phe Leu  
 290 295 300  
 Thr Ala Gly Pro Ser Ala Phe Asn Ile Thr Ser Leu Ile Ser Gln Ala  
 305 310 315 320  
 Ala Gln Leu Ser Thr Gln Ala Gln Pro Ser Asn Gln Ser Pro Met Ser  
 325 330 335  
 Leu Thr Ser Asp Ala Ser Ser Pro Arg Ser Tyr Val Ser Pro Arg Ile  
 340 345 350  
 Ser Thr Pro Gln Thr Asn Thr Val Pro Ile Lys Pro Leu Ile Ser Thr  
 355 360 365  
 Pro Pro Val Ser Ser Gln Pro Lys Val Ser Thr Pro Val Val Lys Gln  
 370 375 380  
 Gly Pro Val Ser Gln Ser Ala Thr Gln Gln Pro Val Thr Ala Asp Lys  
 385 390 395 400  
 Gln Gln Gly His Glu Pro Val Ser Pro Arg Ser Leu Gln Arg Ser Ser

				405						410						415
Gln	Arg	Ser	Pro	Ser	Pro	Gly	Pro	Asn	His	Thr	Ser	Asn	Ser	Ser	Asn	
			420					425					430			
Ala	Ser	Asn	Ala	Thr	Val	Val	Pro	Gln	Asn	Ser	Ser	Ala	Arg	Ser	Thr	
		435					440					445				
Cys	Ser	Leu	Thr	Pro	Ala	Leu	Ala	Ala	His	Phe	Ser	Glu	Asn	Leu	Ile	
		450				455					460					
Lys	His	Val	Gln	Gly	Trp	Pro	Ala	Asp	His	Ala	Glu	Lys	Gln	Ala	Ser	
465					470					475					480	
Arg	Leu	Arg	Glu	Glu	Ala	His	Asn	Met	Gly	Thr	Ile	His	Met	Ser	Glu	
				485					490						495	
Ile	Cys	Thr	Glu	Leu	Lys	Asn	Leu	Arg	Ser	Leu	Val	Arg	Val	Cys	Glu	
			500					505					510			
Ile	Gln	Ala	Thr	Leu	Arg	Glu	Gln	Arg	Ile	Leu	Phe	Leu	Arg	Gln	Gln	
		515					520						525			
Ile	Lys	Glu	Leu	Glu	Lys	Leu	Lys	Asn	Gln	Asn	Ser	Phe	Met	Val		
		530				535					540					

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1755 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

CAGTGGAGTC TGTACTGGCT GCGGGGGACC CTGCTCATTT GAAAATCTGA CATCAGCTGG	60
GCAGTCGCCC CCCTCCTCCT TTCCTCCCTC TACTCTGACA CAGCACTTAG CACCTGAATC	120
TTCGTTTCTC TCCAGGGAC CCTCCATTTT CCATATCCAG GAAAATGTGA TGCGCCACAG	180
GTATCAGCGT CTGGATCGCC ACTTCACGTT TTAGCCACAA GTGACTCAGT GGAAGATCCA	240
GAGTCAACAG AGGCTCGTCA GGAAGATGTC TACAGAAAAG GTAGACCAA AGGAGGAAGC	300
TGGGGAAAAA GAGGTGTGCG GAGACCAGAT CAARGGACCG GACAAAGAGG AGGAACCACC	360
AGCTGCTGCA TCCCATGGCC AGGGGTGGCG TCCAGGTGGC AGAGCAGCTA GGAACGCAAG	420
GCCTGAACCT GGGGCCAGAC ACCCTGCTCT CCCGGCCATG GTCAACGACC CTCCAGTACC	480
TGCCTTACTG TGGGCCCAGG AGGTGGGCCA AGTCTTGGCA GGCCGTGCCC GCAGGCTGCT	540

GCTGCAGTTT GGGGTGCTCT TCTGCACCAT CCTCCTTTTG CTCTGGGTGT CTGTCTTCCT	600
CTATGGCTCC TTCTACTATT CCTATATGCC GACAGTCAGC CACCTCAGCC CTGTGCATTT	660
CTACTACAGG ACCGACTGTG ATTCCTCCAC CACCTCACTC TGCTCCTTCC CTGTTGCCAA	720
TGTCTCGCTG ACTAAGGGTG GACGTGATCG GGTGCTGATG TATGGACAGC CGTATCGTGT	780
TACCTTAGAG CTTGAGCTGC CAGAGTCCCC TGTGAATCAA GATTGGGGCA TGTTCTTGGT	840
CACCATTTCC TGCTACACCA GAGGTGGCCG AATCATCTCC ACTTCTTCGC GTTCGGTGAT	900
GCTGCATTAC CGCTCAGACC TGCTCCAGAT GCTGGACACA CTGGTCTTCT CTAGCCTCCT	960
GCTATTTGGC TTTGCAGAGC AGAAGCAGCT GCTGGAGGTG GAACTCTACG CAGACTATAG	1020
AGAGAACTCG TACGTGCCGA CCACTGGAGC GATCATTGAG ATCCACAGCA AGCGCATCCA	1080
GCTGTATGGA GCCTACCTCC GCATCCACGC GCACTTCACT GGGCTCAGAT ACCTGCTATA	1140
CAACTTCCCG ATGACCTGCG CCTTCATAGG TGTTGCCAGC AACTTCACCT TCCTCAGCGT	1200
CATCGTGCTC TTCAGCTACA TGCAGTGGGT GTGGGGGGGC ATCTGGCCCC GACACCGCTT	1260
CTCTTTGCAG GTTAACATCC GAAAAAGAGA CAATTCCCGG AAGGAAGTCC AACGAAGGAT	1320
CTCTGCTCAT CAGCCAGGGC CTGAAGGCCA GGAGGAGTCA ACTCCGCAAT CAGATGTTAC	1380
AGAGGATGGT GAGAGCCCTG AAGATCCCTC AGGGACAGAG GGTCAGCTGT CCGAGGAGGA	1440
GAAACCAGAT CAGCAGCCCC TGAGCGGAGA AGAGGAGCTA GAGCCTGAGG CCAGTGATGG	1500
TTCAGGCTCC TGGGAAGATG CAGCTTTGCT GACGGAGGCC AACCTGCCTG CTCCTGCTCC	1560
TGCTTCTGCT TCTGCCCCTG TCCTAGAGAC TCTGGGCAGC TCTGAACCTG CTGGGGGTGC	1620
TCTCCGACAG CGCCCCACCT GCTCTAGTTC CTGAAGAAAA GGGGCAGACT CCTCACATTC	1680
CAGCACTTTC CCACCTGACT CCTCTCCCCT CGTTTTTCCT TCAATAAACT ATTTTGTGTC	1740
AAAAAAAAAA AAAAA	1755

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

Met Ser Thr Glu Lys Val Asp Gln Lys Glu Glu Ala Gly Glu Lys Glu  
 1 5 10 15  
 Val Cys Gly Asp Gln Ile Lys Gly Pro Asp Lys Glu Glu Glu Pro Pro  
 20 25 30  
 Ala Ala Ala Ser His Gly Gln Gly Trp Arg Pro Gly Gly Arg Ala Ala  
 35 40 45  
 Arg Asn Ala Arg Pro Glu Pro Gly Ala Arg His Pro Ala Leu Pro Ala  
 50 55 60  
 Met Val Asn Asp Pro Pro Val Pro Ala Leu Leu Trp Ala Gln Glu Val  
 65 70 75 80  
 Gly Gln Val Leu Ala Gly Arg Ala Arg Arg Leu Leu Leu Gln Phe Gly  
 85 90 95  
 Val Leu Phe Cys Thr Ile Leu Leu Leu Leu Trp Val Ser Val Phe Leu  
 100 105 110  
 Tyr Gly Ser Phe Tyr Tyr Ser Tyr Met Pro Thr Val Ser His Leu Ser  
 115 120 125  
 Pro Val His Phe Tyr Tyr Arg Thr Asp Cys Asp Ser Ser Thr Thr Ser  
 130 135 140  
 Leu Cys Ser Phe Pro Val Ala Asn Val Ser Leu Thr Lys Gly Gly Arg  
 145 150 155 160  
 Asp Arg Val Leu Met Tyr Gly Gln Pro Tyr Arg Val Thr Leu Glu Leu  
 165 170 175  
 Glu Leu Pro Glu Ser Pro Val Asn Gln Asp Leu Gly Met Phe Leu Val  
 180 185 190  
 Thr Ile Ser Cys Tyr Thr Arg Gly Gly Arg Ile Ile Ser Thr Ser Ser  
 195 200 205  
 Arg Ser Val Met Leu His Tyr Arg Ser Asp Leu Leu Gln Met Leu Asp  
 210 215 220  
 Thr Leu Val Phe Ser Ser Leu Leu Leu Phe Gly Phe Ala Glu Gln Lys  
 225 230 235 240  
 Gln Leu Leu Glu Val Glu Leu Tyr Ala Asp Tyr Arg Glu Asn Ser Tyr  
 245 250 255  
 Val Pro Thr Thr Gly Ala Ile Ile Glu Ile His Ser Lys Arg Ile Gln  
 260 265 270  
 Leu Tyr Gly Ala Tyr Leu Arg Ile His Ala His Phe Thr Gly Leu Arg  
 275 280 285  
 Tyr Leu Leu Tyr Asn Phe Pro Met Thr Cys Ala Phe Ile Gly Val Ala  
 290 295 300

Ser	Asn	Phe	Thr	Phe	Leu	Ser	Val	Ile	Val	Leu	Phe	Ser	Tyr	Met	Gln	
305					310					315					320	
Trp	Val	Trp	Gly	Gly	Ile	Trp	Pro	Arg	His	Arg	Phe	Ser	Leu	Gln	Val	
			325						330					335		
Asn	Ile	Arg	Lys	Arg	Asp	Asn	Ser	Arg	Lys	Glu	Val	Gln	Arg	Arg	Ile	
			340					345					350			
Ser	Ala	His	Gln	Pro	Gly	Pro	Glu	Gly	Gln	Glu	Glu	Ser	Thr	Pro	Gln	
		355					360					365				
Ser	Asp	Val	Thr	Glu	Asp	Gly	Glu	Ser	Pro	Glu	Asp	Pro	Ser	Gly	Thr	
	370					375					380					
Glu	Gly	Gln	Leu	Ser	Glu	Glu	Glu	Lys	Pro	Asp	Gln	Gln	Pro	Leu	Ser	
385					390					395					400	
Gly	Glu	Glu	Glu	Leu	Glu	Pro	Glu	Ala	Ser	Asp	Gly	Ser	Gly	Ser	Trp	
				405					410					415		
Glu	Asp	Ala	Ala	Leu	Leu	Thr	Glu	Ala	Asn	Leu	Pro	Ala	Pro	Ala	Pro	
			420					425					430			
Ala	Ser	Ala	Ser	Ala	Pro	Val	Leu	Glu	Thr	Leu	Gly	Ser	Ser	Glu	Pro	
		435					440					445				
Ala	Gly	Gly	Ala	Leu	Arg	Gln	Arg	Pro	Thr	Cys	Ser	Ser	Ser			
	450					455					460					

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

GGAATAGAGG	ATTTCAAAAA	GCATGCGTTT	TTTGAAGGTC	TAAATTGGGA	AAATATACGA	60
AACCTAGAAG	CACCTTATAT	TCCTGATGTG	AGCAGTCCCT	CTGACACATC	CAACTTCGAC	120
GTGGATGACG	ACGTGCTGAG	AAACACGGAA	ATATTACCTC	CTGGTTCTCA	CACAGGCTTT	180
TCTGGATTAC	ATTTGCCATT	CATTGGTTTT	ACATTCACAA	CGGAAAGCTG	TTTTTCTGAT	240
CGAGGCTCTC	TGAAGAGCAT	AATGCAGTCC	AACACATTAA	CCAAAGATGA	GGATGTGCAG	300
CGGGACCTGG	AGCACAGCCT	GCAGATGGAA	GCTTACGAGA	GGAGGATTCG	GAGGCTGGAA	360
CAGGAGAAGC	TGGAGCTGAG	CAGGAAGCTG	CAAGAGTCCA	CCCAGACCGT	GCAGTCCCTC	420



CACGGCTCAT	CTCGGGCCCT	CAGCAATTCA	AACCGAGATA	AAGAAATCAA	AAAGCTAAAT	480
GAAGAAATCG	AACGCTTGAA	GAATAAAATA	GCAGATTCAA	ACAGGCTGGA	GCGACAGCTT	540
GAGGACACAG	TGGCGCTTCG	CCAAGAGCGT	GAGGACTCCA	CGCAGCGGCT	GCGGGGGCTG	600
GAGAAGCAGC	ACCGCGTGGT	CCGGCAGGAG	AAGGAGGAGC	TGCACAAGCA	ACTGGTTGAA	660
GCCTCAGAGC	GGTTGAAATC	CCAGGCCAAG	GAACTCAAAG	ATGCCCATCA	GCAGCGAAAAG	720
CTGGCCCTGC	AGGAGTTCTC	GGAGCTGAAC	GAGCGCATGG	CAGAGCTCCG	TGCCCAGAAG	780
CAGAAGGTGT	CCCGGCAGCT	GCGAGACAAG	GAGGAGGAGA	TGGAGGTGGC	CACGCAGAAG	840
GTGGACGCCA	TGCGGCAGGA	AATGCGGAGA	GCTGAGAAGC	TCAGGAAAGA	GCTGGAAGCT	900
CAGCTTGATG	ATGCTGTTGC	TGAGGCCTCC	AAGGAGCGCA	AGCTTCGTGA	GCACAGCGAG	960
AACTTCTGCA	AGCAAATGGA	AAGCGAGCTG	GAGGCCCTCA	AGGTGAAGCA	AGGAGGCCGG	1020
GGAGCGGGTG	CCACCTTAGA	GCACCAGCAA	GAGATTTCCT	AAATCAAATC	CGAGCTGGAG	1080
AAGAAAGTCT	TATTTTATGA	AGAGGAATTG	GTCAGACGTG	AGGCCTCCCA	TGTGCTAGAA	1140
GTGAAAAATG	TGAAGAAGGA	GGTGCATGAT	TCAGAAAAGC	ACCAGCTGGC	CCTGCAGAAA	1200
GAAATCTTGA	TGTTAAAAGA	TAAGTTAGAA	AAGTCAAAGC	GAGAACGGCA	TAACGAGATG	1260
GAGGAGGCAG	TAGGTACAAT	AAAAGATAAA	TACGAACGAG	AAAGAGCGAT	GCTGTTTGAT	1320
GAAAACAAGA	AGCTAACTGC	TGAAAATGAA	AAGCTCTGTT	CCTTTGTGGA	TAAACTCACA	1380
GCTCAAAAATA	GACAGCTGGA	GGATGAGCTG	CAGGATCTGG	CAGCCAAGAA	GGAGTCAGTG	1440
GCCCCACTGGG	AAGCTCAGAT	TGCGGAAATC	ATTCAGTGGG	TCAGTGACGA	GAAAGATGCC	1500
CGGGGTTACC	TTCAAGCTCT	TGCTTCCAAG	ATGACCGAAG	AGCTCGAGGC	TTTGAGGAGT	1560
TCTAGTCTGG	GGTCAAGAAC	ACTGGACCCG	CTGTGGAAGG	TGCGCCGCAG	CCAGAAGCTG	1620
GACATGTCCG	CGCGGCTGGA	GCTGCAGTCG	GCCCTGGAGG	CGGAGATCCG	GGCCAAGCAG	1680
CTTGTCCAGG	AGGAGCTCAG	GAAGGTCAAG	GACGCCAACC	TCACCTTGGA	AAGCAAACYA	1740
AWGGATTCCG	AAGCCAAAAA	CAGAGAATTA	TTAGAAGAAA	TGGAATTTT	GAAGAAAAAG	1800
ATGGAAGAAA	AATTCAGAGC	AGATACTGGG	CTCAAACCTC	CAGATTTTCA	GGATTCCATT	1860
TTTGAGTATT	TCAACACTGC	TCCTCTTGCA	CATGACCTGA	CATTTAGAAC	CAGCTCAGCT	1920
AGTGAGCAAG	AAACACAAGC	TCCGAAGCCA	GAAGCGTCCC	CGTCGATGTC	TGTGGCTGCA	1980
TCAGAGCAGC	AGGAGGACAT	GGCTCGGCCC	CCGCAGAGGC	CATCCGCTGT	GCCGTTGCCC	2040
ACCACGCAGG	CCCTGGCTCT	GGCTGGACCG	AAGCCAAAAG	CTCACCAGTT	CAGCATCAAG	2100

TCCTTCTCCA GCCCTACTCA GTGCAGCCAC TGCACCTCCC TGATGGTTGG GCTGATCCGG	2160
CAGGGCTACG CCTGCGAGGT GTGTTTCCTTT GCTTGCCACG TGTCTGCAA AGACGGTGCC	2220
CCCCAGGTGT GCCCAATACC TCCCAGCAG TCCAAGAGGC CTCTGGGCGT GGACGTGCAG	2280
CGAGGCATCG GAACAGCCTA CAAAGGCCAT GTCAAGGTCC CAAAGCCCAC GGGGGTGAAG	2340
AAGGGATGGC AGCGCGCATA TGCAGTCGTC TGTGACTGCA AGCTCTTCCT GTATGATCTG	2400
CCTGAAGGAA AATCCACCCA GCCTGGTGTC ATTGCGAGCC AAGTCTTGGA TCTCAGAGAT	2460
GACGAGTTTT CCGTGAGCTC AGTCCTGGCC TCAGATGTCA TTCATGCTAC ACGCCGAGAT	2520
ATTCCATGTA TATTCAGGGT GACGGCCTCT CTCTTAGGTG CACCTTCTAA GACCAGCTCG	2580
CTGCTCATTC TGACAGAAAA TGAGAATGAA AAGAGGAAGT GGGTTGGGAT TCTAGAAGGA	2640
CTCCAGTCCA TCCTTCATAA AAACCGGCTG AGGAATCAGG TCGTGCATGT TCCCTTGGA	2700
GCCTACGACA GCTCGCTGCC TCTCATCAAG GCCATCCTGA CAGCTGCCAT CGTGGATGCA	2760
GACAGGATTG CAGTCGGCCT AGAAGAAGGG CTCTATGTCA TAGAGGTCAC CCGAGATGTG	2820
ATCGTCCGTG CCGCTGACTG TAAGAAGGTA CACCAGATCG AGCTTGCTCC CAGGGAGAAG	2880
ATCGTAATCC TCCTCTGTGG CCGGAACCAC CATGTGCACC TCTATCCGTG GTCGTCCCTT	2940
GATGGAGCGG AAGGCAGCTT TGACATCAAG CTTCCGGAAA CCAAAGGCTG CCAGCTCATG	3000
GCCACGGCCA CACTCAAGAG GARCTCTGGC ACCTGCCTGT TTGTGGCCGT GAAACGGCTG	3060
ATCCTTTGCT ATGAGATCCA GAAAATAAAG CCATATTGAA TGATAAAAAA AAAAAAAAAA	3120
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	3180
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAA	3213

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 945 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

Met	Gln	Ser	Asn	Thr	Leu	Thr	Lys	Asp	Glu	Asp	Val	Gln	Arg	Asp	Leu
1				5				10						15	

Glu	His	Ser	Leu	Gln	Met	Glu	Ala	Tyr	Glu	Arg	Arg	Ile	Arg	Arg	Leu
			20					25						30	

Glu Gln Glu Lys Leu Glu Leu Ser Arg Lys Leu Gln Glu Ser Thr Gln  
 35 40 45  
 Thr Val Gln Ser Leu His Gly Ser Ser Arg Ala Leu Ser Asn Ser Asn  
 50 55 60  
 Arg Asp Lys Glu Ile Lys Lys Leu Asn Glu Glu Ile Glu Arg Leu Lys  
 65 70 75 80  
 Asn Lys Ile Ala Asp Ser Asn Arg Leu Glu Arg Gln Leu Glu Asp Thr  
 85 90 95  
 Val Ala Leu Arg Gln Glu Arg Glu Asp Ser Thr Gln Arg Leu Arg Gly  
 100 105 110  
 Leu Glu Lys Gln His Arg Val Val Arg Gln Glu Lys Glu Glu Leu His  
 115 120 125  
 Lys Gln Leu Val Glu Ala Ser Glu Arg Leu Lys Ser Gln Ala Lys Glu  
 130 135 140  
 Leu Lys Asp Ala His Gln Gln Arg Lys Leu Ala Leu Gln Glu Phe Ser  
 145 150 155 160  
 Glu Leu Asn Glu Arg Met Ala Glu Leu Arg Ala Gln Lys Gln Lys Val  
 165 170 175  
 Ser Arg Gln Leu Arg Asp Lys Glu Glu Glu Met Glu Val Ala Thr Gln  
 180 185 190  
 Lys Val Asp Ala Met Arg Gln Glu Met Arg Arg Ala Glu Lys Leu Arg  
 195 200 205  
 Lys Glu Leu Glu Ala Gln Leu Asp Asp Ala Val Ala Glu Ala Ser Lys  
 210 215 220  
 Glu Arg Lys Leu Arg Glu His Ser Glu Asn Phe Cys Lys Gln Met Glu  
 225 230 235 240  
 Ser Glu Leu Glu Ala Leu Lys Val Lys Gln Gly Gly Arg Gly Ala Gly  
 245 250 255  
 Ala Thr Leu Glu His Gln Gln Glu Ile Ser Lys Ile Lys Ser Glu Leu  
 260 265 270  
 Glu Lys Lys Val Leu Phe Tyr Glu Glu Glu Leu Val Arg Arg Glu Ala  
 275 280 285  
 Ser His Val Leu Glu Val Lys Asn Val Lys Lys Glu Val His Asp Ser  
 290 295 300  
 Glu Ser His Gln Leu Ala Leu Gln Lys Glu Ile Leu Met Leu Lys Asp  
 305 310 315 320  
 Lys Leu Glu Lys Ser Lys Arg Glu Arg His Asn Glu Met Glu Glu Ala  
 325 330 335

Val	Gly	Thr	Ile	Lys	Asp	Lys	Tyr	Glu	Arg	Glu	Arg	Ala	Met	Leu	Phe	340	345	350
Asp	Glu	Asn	Lys	Lys	Leu	Thr	Ala	Glu	Asn	Glu	Lys	Leu	Cys	Ser	Phe	355	360	365
Val	Asp	Lys	Leu	Thr	Ala	Gln	Asn	Arg	Gln	Leu	Glu	Asp	Glu	Leu	Gln	370	375	380
Asp	Leu	Ala	Ala	Lys	Lys	Glu	Ser	Val	Ala	His	Trp	Glu	Ala	Gln	Ile	385	390	395
Ala	Glu	Ile	Ile	Gln	Trp	Val	Ser	Asp	Glu	Lys	Asp	Ala	Arg	Gly	Tyr	405	410	415
Leu	Gln	Ala	Leu	Ala	Ser	Lys	Met	Thr	Glu	Glu	Leu	Glu	Ala	Leu	Arg	420	425	430
Ser	Ser	Ser	Leu	Gly	Ser	Arg	Thr	Leu	Asp	Pro	Leu	Trp	Lys	Val	Arg	435	440	445
Arg	Ser	Gln	Lys	Leu	Asp	Met	Ser	Ala	Arg	Leu	Glu	Leu	Gln	Ser	Ala	450	455	460
Leu	Glu	Ala	Glu	Ile	Arg	Ala	Lys	Gln	Leu	Val	Gln	Glu	Glu	Leu	Arg	465	470	475
Lys	Val	Lys	Asp	Ala	Asn	Leu	Thr	Leu	Glu	Ser	Lys	Xaa	Xaa	Asp	Ser	485	490	495
Glu	Ala	Lys	Asn	Arg	Glu	Leu	Leu	Glu	Glu	Met	Glu	Ile	Leu	Lys	Lys	500	505	510
Lys	Met	Glu	Glu	Lys	Phe	Arg	Ala	Asp	Thr	Gly	Leu	Lys	Leu	Pro	Asp	515	520	525
Phe	Gln	Asp	Ser	Ile	Phe	Glu	Tyr	Phe	Asn	Thr	Ala	Pro	Leu	Ala	His	530	535	540
Asp	Leu	Thr	Phe	Arg	Thr	Ser	Ser	Ala	Ser	Glu	Gln	Glu	Thr	Gln	Ala	545	550	555
Pro	Lys	Pro	Glu	Ala	Ser	Pro	Ser	Met	Ser	Val	Ala	Ala	Ser	Glu	Gln	565	570	575
Gln	Glu	Asp	Met	Ala	Arg	Pro	Pro	Gln	Arg	Pro	Ser	Ala	Val	Pro	Leu	580	585	590
Pro	Thr	Thr	Gln	Ala	Leu	Ala	Leu	Ala	Gly	Pro	Lys	Pro	Lys	Ala	His	595	600	605
Gln	Phe	Ser	Ile	Lys	Ser	Phe	Ser	Ser	Pro	Thr	Gln	Cys	Ser	His	Cys	610	615	620
Thr	Ser	Leu	Met	Val	Gly	Leu	Ile	Arg	Gln	Gly	Tyr	Ala	Cys	Glu	Val	625	630	635

Cys	Ser	Phe	Ala	Cys	His	Val	Ser	Cys	Lys	Asp	Gly	Ala	Pro	Gln	Val	645	650	655
Cys	Pro	Ile	Pro	Pro	Glu	Gln	Ser	Lys	Arg	Pro	Leu	Gly	Val	Asp	Val	660	665	670
Gln	Arg	Gly	Ile	Gly	Thr	Ala	Tyr	Lys	Gly	His	Val	Lys	Val	Pro	Lys	675	680	685
Pro	Thr	Gly	Val	Lys	Lys	Gly	Trp	Gln	Arg	Ala	Tyr	Ala	Val	Val	Cys	690	695	700
Asp	Cys	Lys	Leu	Phe	Leu	Tyr	Asp	Leu	Pro	Glu	Gly	Lys	Ser	Thr	Gln	705	710	715
Pro	Gly	Val	Ile	Ala	Ser	Gln	Val	Leu	Asp	Leu	Arg	Asp	Asp	Glu	Phe	725	730	735
Ser	Val	Ser	Ser	Val	Leu	Ala	Ser	Asp	Val	Ile	His	Ala	Thr	Arg	Arg	740	745	750
Asp	Ile	Pro	Cys	Ile	Phe	Arg	Val	Thr	Ala	Ser	Leu	Leu	Gly	Ala	Pro	755	760	765
Ser	Lys	Thr	Ser	Ser	Leu	Leu	Ile	Leu	Thr	Glu	Asn	Glu	Asn	Glu	Lys	770	775	780
Arg	Lys	Trp	Val	Gly	Ile	Leu	Glu	Gly	Leu	Gln	Ser	Ile	Leu	His	Lys	785	790	795
Asn	Arg	Leu	Arg	Asn	Gln	Val	Val	His	Val	Pro	Leu	Glu	Ala	Tyr	Asp	805	810	815
Ser	Ser	Leu	Pro	Leu	Ile	Lys	Ala	Ile	Leu	Thr	Ala	Ala	Ile	Val	Asp	820	825	830
Ala	Asp	Arg	Ile	Ala	Val	Gly	Leu	Glu	Glu	Gly	Leu	Tyr	Val	Ile	Glu	835	840	845
Val	Thr	Arg	Asp	Val	Ile	Val	Arg	Ala	Ala	Asp	Cys	Lys	Lys	Val	His	850	855	860
Gln	Ile	Glu	Leu	Ala	Pro	Arg	Glu	Lys	Ile	Val	Ile	Leu	Leu	Cys	Gly	865	870	875
Arg	Asn	His	His	Val	His	Leu	Tyr	Pro	Trp	Ser	Ser	Leu	Asp	Gly	Ala	885	890	895
Glu	Gly	Ser	Phe	Asp	Ile	Lys	Leu	Pro	Glu	Thr	Lys	Gly	Cys	Gln	Leu	900	905	910
Met	Ala	Thr	Ala	Thr	Leu	Lys	Arg	Xaa	Ser	Gly	Thr	Cys	Leu	Phe	Val	915	920	925
Ala	Val	Lys	Arg	Leu	Ile	Leu	Cys	Tyr	Glu	Ile	Gln	Lys	Ile	Lys	Pro	930	935	940

Tyr  
945

(2) INFORMATION FOR SEQ ID NO:192:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 1315 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

GAGGGCACTT AATCCCAATG AACTGTATGC TTAAAAATAA TTAAATGAT AAAC TTTGTG	60
TTATGTATAC TTTACCACAA TAAGAAAAAG TATTTTAGTA CTAGTGGTAA ATAGTTT TTA	120
TTTAATAGAC TTATATTTTA AAGCTTAAAA ATAATTTAGC TTCTAGAGTA TTACGTTTTT	180
CTTCATGGGA ACTTCAAAAA GCAAGTCACT AAATCCAAGA ATTTTAAAGA AAAAACCCAA	240
ATACATGATT TATGCTGCAT CTGGTATAGA TTTTAAAAAG ACTAGTCAAT CTAAGCTCTA	300
AACTATTAAA TGACAAACCA TTTCATATGT CATTGCATAT TCCTATGTAC CACATTCTCA	360
TATTTCTGTT ATGGGCATGA AGGGGTGTTT GATGCTTCCA TGCCATAATA ACCATGACTA	420
TCACAACCAT TGAAATAAAG GTTCTTGCAG TATTTTCAGG ATGGTCCCAG AAATTTAAAT	480
TAATCTCTCA TCCATTGGCT TTTGCTACTT TAGGTTAATA TTAAATATA ACATACATTT	540
TTGGGGTTTA TGCTGTTAGC TCCAAACCAA AAGATTTTGG AAATTTATTT TGGAAATTTT	600
GTGTTTAGAA TATGAATAAA TCTGCTTATT CAGAAAAATT AAACCTTGAT AACTTGGGAC	660
CTCCTATTCC TGTATGTTCT CTGACATACA TTGAGGGATT TGGCTCTCTT TTGTTTATTT	720
GTTTTACTAG TCAGACATTC CTTTGGCTGC CCATACTTAA TTCTGTTGGG TGTTTCCGCC	780
CCCGCCCTCA GCTTCTGCAG CTACTCTGAT CAACATCCGC AATGCCAGGA AACACTTTGA	840
AAAGCTGGAA AGAGTGGATG GACCAAAGCA GTGTCTTCTC ATGCGCTAAA CATTGATGAA	900
TATTGTTTCA CACAAAAATT AAAAGTTTCC TAATTAATGT TGTATTCATA TATGTAGGCT	960
CTGAAATGTT GTGATGCTTA TTGCTTCTGT ATTTCTTCTC TACTCCCTAG TCTTAATGTT	1020
TAACCTTGAA TGCTATTAAC TTAAATAGCC ATTGAGGAGT TAGAAGATGA ATTGTTTCATG	1080
AAGTCGGTGT TACATAAAAG TAGGTGATAT GTAAGTTTTT TGATAACAAG GTTCTAATAG	1140
TGTTTAAATG TACTGGTAAC CTGGTTCCAA TAGTTGTGTT TGCCCAAGCC TTTCTCGGCA	1200
TCATCTTGTA TTCCTTATCA GATAGTAAGT AACCTGTAAAG TTTGGAGTAT TACTGTTTTT	1260
TCAGCATGCA TTAAAAATAT TCCTTAACTT CAATTGTAAA AAAAAAAAAA AAAAA	1315

*[Redacted]*

(A) LENGTH: 65 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

Leu  
65

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 519 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

TAGGCCATGA	AGGCCGAATC	GGCCTTCATG	GCCTACGCTT	ACACAATACC	CACCATGTCC	60
CAGGCTGGTG	CTCAGGAAGC	CCCTATCAAG	AAGAAGCGCC	CCCCTGTGAA	GGAGGAGGAC	120
CTGAAGGGGG	CCCGAGGAAA	CCTGACCAAG	AACCAGGAAA	TCAAGTCCAA	GACCTACCAG	180
GTCATGCGAG	AGTGTGAGCA	AGCTGGCTCG	GCCGCCCCGT	CGGTGTTTCT	CCGCACCCGC	240
ACAGGTACCG	AGACTGTCTT	TGAGAAGCCC	AAAGCCGGAC	CCACCAAGAG	TGTCTTCGGC	300
TGAGAAGTGT	GCGCCACTCC	CCTTGCTGCC	CGAATGCTCG	GAAACAGGAG	CCTTACCCAG	360
GAACTCTTTT	TTATGCCAGA	ACGCTTCCTC	TCCCCTGCTG	TCTCTGGGGC	TGCCACCCTC	420

CCCCACAGTC CAGGCCCTTC AGCCAAGGGC TCTGCACCAG CACCTTGGA GCACCAATAA 480  
AGAGGATGCC CACGTGGCCC CAGCAAAAAA AAAAAAAAAA 519

(2) INFORMATION FOR SEQ ID NO:195:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 98 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

Met Lys Ala Glu Ser Ala Phe Met Ala Tyr Ala Tyr Thr Ile Pro Thr  
 1 5 10 15  
 Met Ser Gln Ala Gly Ala Gln Glu Ala Pro Ile Lys Lys Lys Arg Pro  
 20 25 30  
 Pro Val Lys Glu Glu Asp Leu Lys Gly Ala Arg Gly Asn Leu Thr Lys  
 35 40 45  
 Asn Gln Glu Ile Lys Ser Lys Thr Tyr Gln Val Met Arg Glu Cys Glu  
 50 55 60  
 Gln Ala Gly Ser Ala Ala Pro Ser Val Phe Ser Arg Thr Arg Thr Gly  
 65 70 75 80  
 Thr Glu Thr Val Phe Glu Lys Pro Lys Ala Gly Pro Thr Lys Ser Val  
 85 90 95  
 Phe Gly

(2) INFORMATION FOR SEQ ID NO:196:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2788 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

GACGGCGACC AAACCCAGCT AGGTCAGACG AGAAAGATAA AACTCTCCA GATGTCTTCC 60  
 AGTAATGTCTG AAGTTTTTAT CCCAGTGTCA CAAGGAAACA CCAATGGCTT CCCC GCGACA 120  
 GCTTCCAATG ACCTGAAGGC ATTTACTGAA GGAGCTGTGT TAAGTTTTCA TAACATCTGC 180



TATCGAGTAA	AACTGAAGAG	TGGCTTTCTA	CCTTGTCGAA	AACCAGTTGA	GAAAGAAATA	240
TTATCGAATA	TCAATGGGAT	CATGAAACCT	GGTCTCAACG	CCATCCTGGG	ACCCACAGGT	300
GGARGCAAAT	CTTCGTTATT	AGATGTCTTA	GCTGCAAGGA	AAGATCCAAG	TGGATTATCT	360
GGAGATGTTC	TGATAAATGG	AGCACCGCGA	CCTGCCAATT	TCAAATGTAA	TTCAGGTTAC	420
GTGGTACAAG	TTGGAACCTCA	GTTTATCCGT	GGTGTGTCTG	GAGGAGAAAAG	AAAAAGGACT	480
AGTATAGGAA	TGGAGCTTAT	CACTGATCCT	TCCATCTTGT	TCTTGGATGA	GCCTACAACT	540
GGCTTAGACT	CAAGCACAGC	AAATGCTGTC	CTTTTGCTCC	TGAAAAGGAT	GTCTAAGCAG	600
GGACGAACAA	TCATCTTCTC	CATTCATCAG	CCTCGATATT	CCATCTTCAA	GTTGTTTGAT	660
AGCCTCACCT	TATTGGCCTC	AGGAAGACTT	ATGTTCCACG	GGCCTGCTCA	GGAGGCCTTG	720
GGATACTTTG	AATCAGCTGG	TTATCACTGT	GAGGCCTATA	ATAACCTGTC	AGACTTCTTC	780
TTGGACATCA	TTAATGGAGA	TTCCACTGCT	GTGGCATTAA	ACAGAGAAGA	AGACTTTAAA	840
GCCACAGAGA	TCATAGAGCC	TTCCAAGCAG	GATAAGCCAC	TCATAGAAAA	ATTAGCGGAG	900
ATTTATGTCA	ACTCCTCCTT	CTACAAAGAG	ACAAAAGCTG	AATTACATCA	ACTTTCCGGG	960
GGTGAGAAGA	AGAAGAAGAT	CACAGTCTTC	AAGGAGATCA	GCTACACCAC	CTCCTTCTGT	1020
CATCAACTCA	GATGGGTTTC	CAAGCGTTCA	TTCAAAAAC	TGCTGGGTAA	TCCCAGGCC	1080
TCTATAGCTC	AGATCATTTG	CACAGTCGTA	CTGGGACTGG	TTATAGGTGC	CATTTACTTT	1140
GGGCTAAAAA	ATGATTCTAC	TGGAATCCAG	AACAGAGCTG	GGGTTCTCTT	CTTCCTGACG	1200
ACCAACCAGT	GTTTCAGCAG	TGTTTCAGCC	GTGGAACCTC	TTGTGGTAGA	GAAGAAGCTC	1260
TTCATACATG	AATACATCAG	CGGATACTAC	AGAGTGTCAT	CTTATTTTCCT	TGGAAAACCTG	1320
TTATCTGATT	TATTACCCAT	GAGGATGTTA	CCAAGTATTA	TATTTACCTG	TATAGGTGAC	1380
TTCATGTTAG	GATTGAAGCC	AAAGGCAGAT	GCCTTCTTCG	TTATGATGTT	TACCCTTATG	1440
ATGGTGGCTT	ATTCAGCCAG	TTCCATGGCA	CTGGCCATAG	CAGCAGGTCA	GAGTGTGGTT	1500
TCTGTAGCAA	CACTTCTCAT	GACCATCTGT	TTTGTGTTTA	TGATGATTTT	TTCAGGTCTG	1560
TTGGTCAATC	TCACAACCAT	TGCATCTTGG	CTGTCATGGC	TTCAGTACTT	CAGCATTTCCA	1620
CGATATGGAT	TTACGGCTTT	GCAGCATAAT	GAATTTTTTG	GACAAAACCTT	CTGCCCAGGA	1680
CTCAATGCAA	CAGGAAACAA	TCCTTGTAAC	TATGCAACAT	GTAAGGCGA	AGAATATTTG	1740
GTAAAGCAGG	GCATCGATCT	CTCACCTTGG	GGCTTGTGGA	AGAATCACGT	GGCCTTGGCT	1800
TGTATGATTG	TTATTTTCCT	CACAATTGCC	TACCTGAAAT	TGTTATTTCT	TAAAAAATAT	1860

TCTTAAATTT CCCCTTAATT CAGTATGATT TATCCTCACA TAAAAAAGAA GCACTTTGAT	1920
TGAAGTATTC AATCAAGTTT TTTTGGTTGT TTTCTGTTCC CTTGCCATCA CACTGTTGCA	1980
CAGCAGCAAT TGTTTTAAAG AGATACATTT TTAGAAATCA CAACAACTG AATTAAACAT	2040
GAAAGAACCC AAGACATCAT GTATCGCATA TTAGTTAATC TCCTCAGACA GTAACCATGG	2100
GGAAGAAATC TGGTCTAATT TATTAATCTA AAAAAGGAGA ATTGAATTCT GGAAACTCCT	2160
GACAAGTTAT TACTGTCTCT GGCATTTGTT TCCTCATCTT TAAAATGAAT AGGTAGGTTA	2220
GTAGCCCTTC AGTCTTAATA CTTTATGATG CTATGGTTTG CCATTATTTA ATAAATGACA	2280
AATGTATTAA TGCTAAAAA AAAAAAAAAA AGCGGCCTTC ATGGCCTAGA GATTTCAACT	2340
TAACCTTGACC GCTCTGAGCT AAACCTAGCC CCAAACCCAC TCCACCTTAT TACCAGACAA	2400
CCTTAACCAA ACCATTTACC CAAATAAAGT ATAGGCGATA GAAATTGAAA CCTGGCGCAA	2460
TAGATATAGT ACCGCAAGGG AAAGATGAAA AATTATAACC AAGCATAATA TAGCAAGGAC	2520
TAACCCCTAT ACCTTCTGCA TAATGAATTA ACTAGAAATA ACTTTGCAAG GAGAGCCAAA	2580
GCTAAGACCC CCGAAACCAG ACGAGCTACC TAAGAACAGC TAAAAGAGCA CACCCGTCTA	2640
TGTAGCAAAA TAGTGGGAAG ATTTATAGGT AGAGGCGACA AACCTACCGA GCCTGGTGAT	2700
AGCTGGTTGT CCCAGAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	2760
AAAAAAAAAA AAAAAAAAAA AAAAAAAA	2788

(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 604 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

Met	Ser	Ser	Ser	Asn	Val	Glu	Val	Phe	Ile	Pro	Val	Ser	Gln	Gly	Asn
1				5					10					15	
Thr	Asn	Gly	Phe	Pro	Ala	Thr	Ala	Ser	Asn	Asp	Leu	Lys	Ala	Phe	Thr
			20					25					30		
Glu	Gly	Ala	Val	Leu	Ser	Phe	His	Asn	Ile	Cys	Tyr	Arg	Val	Lys	Leu
		35					40					45			
Lys	Ser	Gly	Phe	Leu	Pro	Cys	Arg	Lys	Pro	Val	Glu	Lys	Glu	Ile	Leu
	50					55					60				

Ser Asn Ile Asn Gly Ile Met Lys Pro Gly Leu Asn Ala Ile Leu Gly  
 65 70 75 80  
 Pro Thr Gly Gly Xaa Lys Ser Ser Leu Leu Asp Val Leu Ala Ala Arg  
 85 90 95  
 Lys Asp Pro Ser Gly Leu Ser Gly Asp Val Leu Ile Asn Gly Ala Pro  
 100 105 110  
 Arg Pro Ala Asn Phe Lys Cys Asn Ser Gly Tyr Val Val Gln Val Gly  
 115 120 125  
 Thr Gln Phe Ile Arg Gly Val Ser Gly Gly Glu Arg Lys Arg Thr Ser  
 130 135 140  
 Ile Gly Met Glu Leu Ile Thr Asp Pro Ser Ile Leu Phe Leu Asp Glu  
 145 150 155 160  
 Pro Thr Thr Gly Leu Asp Ser Ser Thr Ala Asn Ala Val Leu Leu Leu  
 165 170 175  
 Leu Lys Arg Met Ser Lys Gln Gly Arg Thr Ile Ile Phe Ser Ile His  
 180 185 190  
 Gln Pro Arg Tyr Ser Ile Phe Lys Leu Phe Asp Ser Leu Thr Leu Leu  
 195 200 205  
 Ala Ser Gly Arg Leu Met Phe His Gly Pro Ala Gln Glu Ala Leu Gly  
 210 215 220  
 Tyr Phe Glu Ser Ala Gly Tyr His Cys Glu Ala Tyr Asn Asn Pro Ala  
 225 230 235 240  
 Asp Phe Phe Leu Asp Ile Ile Asn Gly Asp Ser Thr Ala Val Ala Leu  
 245 250 255  
 Asn Arg Glu Glu Asp Phe Lys Ala Thr Glu Ile Ile Glu Pro Ser Lys  
 260 265 270  
 Gln Asp Lys Pro Leu Ile Glu Lys Leu Ala Glu Ile Tyr Val Asn Ser  
 275 280 285  
 Ser Phe Tyr Lys Glu Thr Lys Ala Glu Leu His Gln Leu Ser Gly Gly  
 290 295 300  
 Glu Lys Lys Lys Lys Ile Thr Val Phe Lys Glu Ile Ser Tyr Thr Thr  
 305 310 315 320  
 Ser Phe Cys His Gln Leu Arg Trp Val Ser Lys Arg Ser Phe Lys Asn  
 325 330 335  
 Leu Leu Gly Asn Pro Gln Ala Ser Ile Ala Gln Ile Ile Val Thr Val  
 340 345 350  
 Val Leu Gly Leu Val Ile Gly Ala Ile Tyr Phe Gly Leu Lys Asn Asp  
 355 360 365

Ser	Thr	Gly	Ile	Gln	Asn	Arg	Ala	Gly	Val	Leu	Phe	Phe	Leu	Thr	Thr	370	375	380	
Asn	Gln	Cys	Phe	Ser	Ser	Val	Ser	Ala	Val	Glu	Leu	Phe	Val	Val	Glu	385	390	395	400
Lys	Lys	Leu	Phe	Ile	His	Glu	Tyr	Ile	Ser	Gly	Tyr	Tyr	Arg	Val	Ser	405	410	415	
Ser	Tyr	Phe	Leu	Gly	Lys	Leu	Leu	Ser	Asp	Leu	Leu	Pro	Met	Arg	Met	420	425	430	
Leu	Pro	Ser	Ile	Ile	Phe	Thr	Cys	Ile	Val	Tyr	Phe	Met	Leu	Gly	Leu	435	440	445	
Lys	Pro	Lys	Ala	Asp	Ala	Phe	Phe	Val	Met	Met	Phe	Thr	Leu	Met	Met	450	455	460	
Val	Ala	Tyr	Ser	Ala	Ser	Ser	Met	Ala	Leu	Ala	Ile	Ala	Ala	Gly	Gln	465	470	475	480
Ser	Val	Val	Ser	Val	Ala	Thr	Leu	Leu	Met	Thr	Ile	Cys	Phe	Val	Phe	485	490	495	
Met	Met	Ile	Phe	Ser	Gly	Leu	Leu	Val	Asn	Leu	Thr	Thr	Ile	Ala	Ser	500	505	510	
Trp	Leu	Ser	Trp	Leu	Gln	Tyr	Phe	Ser	Ile	Pro	Arg	Tyr	Gly	Phe	Thr	515	520	525	
Ala	Leu	Gln	His	Asn	Glu	Phe	Leu	Gly	Gln	Asn	Phe	Cys	Pro	Gly	Leu	530	535	540	
Asn	Ala	Thr	Gly	Asn	Asn	Pro	Cys	Asn	Tyr	Ala	Thr	Cys	Thr	Gly	Glu	545	550	555	560
Glu	Tyr	Leu	Val	Lys	Gln	Gly	Ile	Asp	Leu	Ser	Pro	Trp	Gly	Leu	Trp	565	570	575	
Lys	Asn	His	Val	Ala	Leu	Ala	Cys	Met	Ile	Val	Ile	Phe	Leu	Thr	Ile	580	585	590	
Ala	Tyr	Leu	Lys	Leu	Leu	Phe	Leu	Lys	Lys	Tyr	Ser					595	600		

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2930 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

CGACTTCCTC	GGCTGCGCGG	CGCTCGCGCG	GAGCTCCCCG	GCCGGCGGTG	CGTCCCCACG	60
GTCACCATGA	AAGACGACTT	CGCAGAGGAG	GAGGAGGTGC	AATCCTTCGG	TTACAAGCGG	120
TTTGGTATTC	AGGAAGGAAC	ACAATGTACC	AAATGTAAAA	ATAACTGGGC	ACTGAAGTTT	180
TCTATCATAT	TATTATACAT	TTTGTGTGCC	TTGCTAACAA	TCACAGTAGC	CATTTTGGGA	240
TATAAAGTTG	TAGAGAAAAAT	GGACAATGTC	ACAGGTGGCA	TGGAAACATC	TCGCCAAACC	300
TATGATGACA	AGCTCACAGC	AGTGGAAGT	GACCTGAAAA	AATTAGGTGA	CCAAACTGGG	360
AAGAAAGCTA	TCAGCACCAA	CTCAGAACTC	TCCACCTTCA	GATCAGACAT	TCTAGATCTC	420
CGTCAGCAAC	TTCGTGAGAT	TACAGAAAAA	ACCAGCAAGA	ACAAGGATAC	GCTGGAGAAG	480
TTACAGGCGA	GCGGGGATGC	TCTGGTGGAC	AGGCAGAGTC	AATTGAAAGA	AACTTTGGAG	540
AATAACTCTT	TCCTCATCAC	CACTGTAAAC	AAAACCCCTC	AGGCGTATAA	TGGCTATGTC	600
ACGAATCTGC	AGCAAGATAC	CAGCGTGCTC	CAGGGCAATC	TGCAGAACCA	AATGTATTCT	660
CATAATGTGG	TCATCATGAA	CTCAACAACC	TGAACCTGAC	CCAGGTGCAG	CAGAGGAACC	720
TCATCACGAA	TCTGCAGCGG	TCTGTGGATG	ACACAAGCCA	GGCTATCCAG	CGAATCAAGA	780
ACGACTTTCA	AAATCTGCAG	CAGGTTTTTC	TTCAAGCCAA	GAAGGACACG	GATTGGCTGA	840
AGGAGAAAGT	GCAGAGCTTG	CAGACGCTGG	CTGCCAACAA	CTCTGCGTTG	GCCAAAGCCA	900
ACAACGACAC	CCTGGAGGAT	ATGAACAGCC	AGCTCAACTC	ATTCACAGGT	CAGATGGAGA	960
ACATCACCAC	TATCTCTCAA	GCCAACGAGC	AGAACCTGAA	AGACCTGCAG	GACTTACACA	1020
AAGATGCAGA	GAATAGAACA	GCCATCAAGT	TCAACCAACT	GGAGGAACGC	TTCCAGCTCT	1080
TTGAGACGGA	TATTGTGAAC	ATCATTAGCA	ATATCAGTTA	CACAGCCCAC	CACCTGCGGA	1140
CGCTGACCAG	CAATCTAAAT	GAAGTCAGGA	CCACTTGCAC	AGATACCCTT	ACCAAACACA	1200
CAGATGATCT	GACCTCCTTG	AATAATACCC	TGGCCAACAT	CCGTTTGGAT	TCTGTTTCTC	1260
TCAGGATGCA	ACAAGATTTG	ATGAGGTCGA	GGTTAGACAC	TGAAGTAGCC	AACTTATCAG	1320
TGATTATGGA	AGAAATGAAG	CTAGTAGACT	CCAAGCATGG	TCAGCTCATC	AAGAATTTTA	1380
CAATACTACA	AGGTCCACCG	GGCCCCAGGG	GTCCAAGAGG	TGACAGAGGA	TCCCAGGGAC	1440
CCCCTGGCCC	AACTGGCAAC	AAGGGACAGA	AAGGAGAGAA	GGGGGAGCCT	GGACCACCTG	1500
GCCCTGCGGG	TGAGAGAGGC	CCAATTGGAC	CAGCTGGTCC	CCCCGGAGAG	CGTGGCGGCA	1560
AAGGATCTAA	AGGCTCCCAG	GGCCCCAAAG	GCTCCCCTGG	TTCCCCTGGG	AAGCCCGGCC	1620
CTCAGGGCCC	CAGTGGGGAC	CCAGGCCCCC	CGGGCCCACC	AGGCAAAGAG	GGACTCCCCG	1680

GCCCTCAGGG CCCTCCTGGC TTCCAGGGAC TTCAGGGCAC CGTTGGGGAG CCTGGGGTGC	1740
CTGGACCTCG GGGACTGCCA GGCTTGCCTG GGGTACCAGG CATGCCAGGC CCCAAGGGCC	1800
CCCCCGGCCC TCCTGGCCCA TCAGGAGCGG TGGTGCCCTT GGCCCTGCAG AATGAGCCAA	1860
CCCCGGCACC GGAGGACAAT AGCTGCCCCG CTCACTGGAA GAACTTCACA GACAAATGCT	1920
ACTATTTTTC AGTTGAGAAA GAAATTTTTC AGGATGCAAA GCTTTTCTGT GAAGACAAGT	1980
CTTCACATCT TGTTCATATA AACACTAGAG AGGAACAGCA ATGGATAAAA AAACAGATGG	2040
TAGGGAGAGA GAGCCACTGG ATCGGCCTCA CAGACTCAGA GCGTGAAAAT GAATGGAAGT	2100
GGCTGGATGG GACATCTCCA GACTACAAAA ATTGGAAAGC TGGACAGCCG GATAACTGGG	2160
GTCATGGCCA TGGGCCAGGA GAAGACTGTG CTGGGTTGAT TTATGCTGGG CAGTGGAACG	2220
ATTTCCAATG TGAAGACGTC AATAACTTCA TTTGCGAAAA AGACAGGGAG ACAGTACTGT	2280
CATCTGCATT ATAACGGACT GTGATGGGAT CACATGAGCA AATTTTCAGC TCTCAAAGGC	2340
AAAGGACACT CCTTTCTAAT TGCATCACCT TCTCATCAGA TTGAAAAAAAA AAAAGCACTG	2400
AAAGCCAATT ACTGAAAAA AATTGACAGC TAGTGTTTTT TACCATCCGT CATTACCCAA	2460
AGACTTGGGA ACTAAAATGT TCCCCAGGGT GATATGCTGA TTTTCATTGT GCACATGGAC	2520
TGAATCACAT AGATTCTCCT CCGTCAGTAA CCGTGCGATT ATACAAATTA TGTCTTCCAA	2580
AGTATGGAAC ACTCCAATCA GAAAAAGGTT ATCATTGGTC GTTGAGTTAT GGGAAGAACT	2640
TAAGCATATA CTGTGTAAAC AGTGCCATAC ATTTCTAAAA TCCCAAGTGT AGGAAAAATA	2700
TGCAGACATA CAGATATATA GGCCAACTAT TAGTAATAAT ATGAAATATA CTTAAAGAGC	2760
TTTTAAAACT TTGTATTTTT GTACAAAATA TTTGTCTTTT ACAATTTTTT TCCTTTTTTT	2820
TTTTTTGTCA TTTTACCGAC ATAATACATG GAGCCAAAGA AAACAATAAT GGTACTAATA	2880
AAAACCTCTA GGGTTTCCTG TCAGATTTAA TTCTAAAAA AAAAAAAAAA	2930

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

Met Lys Asp Asp Phe Ala Glu Glu Glu Glu Val Gln Ser Phe Gly Tyr

1	5	10	15
Lys Arg Phe Gly Ile Gln Glu Gly Thr Gln Cys Thr Lys Cys Lys Asn	20	25	30
Asn Trp Ala Leu Lys Phe Ser Ile Ile Leu Leu Tyr Ile Leu Cys Ala	35	40	45
Leu Leu Thr Ile Thr Val Ala Ile Leu Gly Tyr Lys Val Val Glu Lys	50	55	60
Met Asp Asn Val Thr Gly Gly Met Glu Thr Ser Arg Gln Thr Tyr Asp	65	70	75
Asp Lys Leu Thr Ala Val Glu Ser Asp Leu Lys Lys Leu Gly Asp Gln	85	90	95
Thr Gly Lys Lys Ala Ile Ser Thr Asn Ser Glu Leu Ser Thr Phe Arg	100	105	110
Ser Asp Ile Leu Asp Leu Arg Gln Gln Leu Arg Glu Ile Thr Glu Lys	115	120	125
Thr Ser Lys Asn Lys Asp Thr Leu Glu Lys Leu Gln Ala Ser Gly Asp	130	135	140
Ala Leu Val Asp Arg Gln Ser Gln Leu Lys Glu Thr Leu Glu Asn Asn	145	150	155
Ser Phe Leu Ile Thr Thr Val Asn Lys Thr Leu Gln Ala Tyr Asn Gly	165	170	175
Tyr Val Thr Asn Leu Gln Gln Asp Thr Ser Val Leu Gln Gly Asn Leu	180	185	190
Gln Asn Gln Met Tyr Ser His Asn Val Val Ile Met Asn Ser Thr Thr	195	200	205

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1589 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

TCTATATATT TTTTCTAGGA AGGGGTGTTT TTCTTTCTGA TTTAATTCCC TACATTTTTC	60
TCTTTCATAT GAAGTTGCAG ATAATGTTTT TCCTTCGGAT TTTTATTCTT TAAGATTTTT	120
AACCTGTGCA AGACTTTTTC AATGATACAA GTCAAGGAGG ATGAAGATCT TTTTCCACTT	180

CAGTCTTCAC	TTTGCTCCAG	CTATTGCTAA	GAAAGGCACA	AACAATGACA	GCATATTTAA	240
GGAAGAACCT	GGCCGGCTTG	GGTCACCGCT	GCTGTCTTTC	TTGGTTTTGC	GTCTACCTGG	300
GAGAGCCCAG	CTTTTAGGTT	CCCATTGAGG	GAAGCATGAG	AGAGGATTGT	TTGGGGGATG	360
CTGCCAGAGC	TTCCAGCTGA	CAGTCTCTGC	AGAGCGGCTG	CCAAGTGGCC	TGGTGGCCGT	420
ATGTTGGCAG	TTTTTGATGA	ATTGGGATTA	GGGAATGTTT	GTTTACTTGA	TAACCGAGTG	480
TCTACAAGGA	GAGGTGGCAG	CGTGAGGGAA	TAGTGCCACC	ATAATGAGGA	CACAGCCAGC	540
CATCTCTTCC	CTGCCACAGA	ACCCAGGCA	GTCCCCTTCA	GGCTACAGTT	TTCCATCTGG	600
ACCGAGGGAC	TGGCCGGTGC	AGCAGGAGGA	GCCGATCACC	CTCTGTGGGA	ACGAGGATGC	660
CCAGAAGTTC	CAGTTACTGT	GGCTCCATGG	TCCCCTTCTC	GATGCGCATC	TTGCACGCGG	720
AGCTTCAGCA	GTACCTGGGG	AACCCACAGG	AGTCGCTGGA	TAGACTGCAC	AAGGTGAAGA	780
CTGTCTGCAG	CAAGATCCTG	GCCAATTTGG	AGCAAGGCTT	AGCAGAAGAC	GGCGGCATGA	840
GCAGCGTGAC	TCAGGAGGGC	AGACAAGCCT	CTATCCGGCT	GTGGAGGTCA	CGTCTGGGCC	900
GGGTGATGTA	CTCCATGGCA	AACTGTCTGC	TCCTGATGAA	GGATTATGTG	CTGGCCGTGG	960
AGGCGTATCA	TTCGGTTATC	AAGTATTACC	CAGAGCAAGA	GCCCCAGCTG	CTCAGCGGCA	1020
TCGGCCGGAT	TTCCCTGCAG	ATTGGAGACA	TAAAAACAGC	TGAAAAGTAT	TTCAAGACG	1080
TTGAGAAAGT	AACACAGAAA	TTAGATGGAC	TACAGGGTAA	AATCATGGTT	TTGATGAACA	1140
GCGCGTTTCT	TCACCTCGGG	CAGAATAACT	TTGCAGAAGC	CCACAGGTTC	TTACAGAGA	1200
TCTTAAGGAT	GGATCCAAGA	AACGCAGTGG	CCAACAACAA	CGCTGCCGTG	TGTCTGCTCT	1260
ACCTGGGCAA	GCTCAAGGAC	TCCCTGCGGC	AGCTGGAGGC	CATGGTCCAG	CAGGACCCCA	1320
GGCACTACCT	GCACGAGAGC	GTGCTCTTCA	ACCTGACCAC	CATGTACGAG	CTGGAGTCCT	1380
CACGGAGCAT	GCAGAAGAAA	CAGGCCCTGC	TGGAGGCTGT	CGCCGGCAAG	GAGGGGGACA	1440
GCTTCAACAC	ACAGTGCCTC	AAGCTGGCCT	AGCTGCCTCC	AACACACTAC	GTCAGAAGGA	1500
CCCGGTCTT	TGAAACTGTG	TCTTGAAGCT	AATGTATTAA	TGTGACATGG	AGGAACTCAA	1560
TAAAACTCCT	GCTTCAAAAA	AAAAAAAAAA				1589

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear



(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

Met Pro Arg Ser Ser Ser Tyr Cys Gly Ser Met Val Pro Phe Ser Met  
1 5 10 15

Arg Ile Leu His Ala Glu Leu Gln Gln Tyr Leu Gly Asn Pro Gln Glu  
20 25 30

Ser Leu Asp Arg Leu His Lys Val Lys Thr Val Cys Ser Lys Ile Leu  
35 40 45

Ala Asn Leu Glu Gln Gly Leu Ala Glu Asp Gly Gly Met Ser Ser Val  
50 55 60

Thr Gln Glu Gly Arg Gln Ala Ser Ile Arg Leu Trp Arg Ser Arg Leu  
65 70 75 80

Gly Arg Val Met Tyr Ser Met Ala Asn Cys Leu Leu Leu Met Lys Asp  
85 90 95

Tyr Val Leu Ala Val Glu Ala Tyr His Ser Val Ile Lys Tyr Tyr Pro  
100 105 110

Glu Gln Glu Pro Gln Leu Leu Ser Gly Ile Gly Arg Ile Ser Leu Gln  
115 120 125

Ile Gly Asp Ile Lys Thr Ala Glu Lys Tyr Phe Gln Asp Val Glu Lys  
130 135 140

Val Thr Gln Lys Leu Asp Gly Leu Gln Gly Lys Ile Met Val Leu Met  
145 150 155 160

Asn Ser Ala Phe Leu His Leu Gly Gln Asn Asn Phe Ala Glu Ala His  
165 170 175

Arg Phe Phe Thr Glu Ile Leu Arg Met Asp Pro Arg Asn Ala Val Ala  
180 185 190

Asn Asn Asn Ala Ala Val Cys Leu Leu Tyr Leu Gly Lys Leu Lys Asp  
195 200 205

Ser Leu Arg Gln Leu Glu Ala Met Val Gln Gln Asp Pro Arg His Tyr  
210 215 220

Leu His Glu Ser Val Leu Phe Asn Leu Thr Thr Met Tyr Glu Leu Glu  
225 230 235 240

Ser Ser Arg Ser Met Gln Lys Lys Gln Ala Leu Leu Glu Ala Val Ala  
245 250 255

Gly Lys Glu Gly Asp Ser Phe Asn Thr Gln Cys Leu Lys Leu Ala  
260 265 270

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1153 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

TATAAAGAGT GACTCTCCTA TGAAGGTAAA GGCCACCCCT CTTCAGTTCC AGTGACTGAG 60  
ATACATTTTT CCAATCCTGG GGGCAAATAC AGACACAGCA AGTTCCTTCT TCCCTTTGGA 120  
AATTTGGCAG CTGCCTTCAC CAGTGAGCAC AAAGCCACAT TTCAAAGGAA ACTGACAAAT 180  
TATCCCCAGC TGCCAGAAGA AGAAATCCTC ACTGGACGGC TTCCTGTTTC CTGTGGTTCA 240  
TTATCTGATT GGCTGCAGGG ATGAAAGTTT TTAAGTTCAT AGGACTGATG ATCCTCCTCA 300  
CCTCTGCGTT TTCAGCCGGT TCAGGACAAA GTCCAATGAC TGTGCTGTGC TCCATAGACT 360  
GGTTCATGGT CACAGTGCAC CCCTTCATGC TAAACAACGA TGTGTGTGTA CACTTTCATG 420  
AACTACACTT GGGCCTGGGT TGCCCCCCTAA ACCATGTTCA GCCACACGCC TACCAGTTCA 480  
CCTACCGTGT TACTGAATGT GGCATCAGGG CCAAAGCTGT CTCTCAGGAC ATGGTTATCT 540  
ACAGCACTGA GATACACTAC TCTTCTAAGG GCACGCCATC TAAGTTTGTG ATCCCAGTGT 600  
CATGTGCTGC CCCCCAAAAG TCCCCATGGC TCACCAAGCC CTGCTCCATG AGAGTAGCCA 660  
GCAAGAGCAG GGCCACAGCC CAGAAGGATG AGAAATGCTA CGAGGTGTTT AGCTTGTCAC 720  
AGTCCAGTCA AAGGCCCAAC TGCGATTGTC CACCTTGTGT CTTCAGTGAA GAAGAGCATA 780  
CCCAGGTCCC TTGTCACCAA GCAGGGGCTC AGGAGGCTCA ACCTCTGCAG CCATCTCACT 840  
TTCTTGATAT TTCTGAGGAT TGGTCTCTTC ACACAGATGA TATGATTGGG TCCATGTGAT 900  
CCTCAGGTTT GGGGTCTCCT GAAGATGCTA TTTCTAGAAT TAGTATATAG TGTACAAATG 960  
TCTGACAAAT AAGTGCTCTT GTGACCCCTCA TGTGAGCACT TTTGAGAAAG AGAAACCTAT 1020  
AGCAACTTCA TGAATTAAGC CTTTTTCTAT ATTTTATAT TCATGTGTAA ACAAAAAATA 1080  
AAATAAAATT CTGATCGCAT AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1140  
AAAAAAAAAA AAA 1153

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 212 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

Met	Lys	Val	Phe	Lys	Phe	Ile	Gly	Leu	Met	Ile	Leu	Leu	Thr	Ser	Ala	1	5	10	15
Phe	Ser	Ala	Gly	Ser	Gly	Gln	Ser	Pro	Met	Thr	Val	Leu	Cys	Ser	Ile	20	25	30	
Asp	Trp	Phe	Met	Val	Thr	Val	His	Pro	Phe	Met	Leu	Asn	Asn	Asp	Val	35	40	45	
Cys	Val	His	Phe	His	Glu	Leu	His	Leu	Gly	Leu	Gly	Cys	Pro	Pro	Asn	50	55	60	
His	Val	Gln	Pro	His	Ala	Tyr	Gln	Phe	Thr	Tyr	Arg	Val	Thr	Glu	Cys	65	70	75	80
Gly	Ile	Arg	Ala	Lys	Ala	Val	Ser	Gln	Asp	Met	Val	Ile	Tyr	Ser	Thr	85	90	95	
Glu	Ile	His	Tyr	Ser	Ser	Lys	Gly	Thr	Pro	Ser	Lys	Phe	Val	Ile	Pro	100	105	110	
Val	Ser	Cys	Ala	Ala	Pro	Gln	Lys	Ser	Pro	Trp	Leu	Thr	Lys	Pro	Cys	115	120	125	
Ser	Met	Arg	Val	Ala	Ser	Lys	Ser	Arg	Ala	Thr	Ala	Gln	Lys	Asp	Glu	130	135	140	
Lys	Cys	Tyr	Glu	Val	Phe	Ser	Leu	Ser	Gln	Ser	Ser	Gln	Arg	Pro	Asn	145	150	155	160
Cys	Asp	Cys	Pro	Pro	Cys	Val	Phe	Ser	Glu	Glu	Glu	His	Thr	Gln	Val	165	170	175	
Pro	Cys	His	Gln	Ala	Gly	Ala	Gln	Glu	Ala	Gln	Pro	Leu	Gln	Pro	Ser	180	185	190	
His	Phe	Leu	Asp	Ile	Ser	Glu	Asp	Trp	Ser	Leu	His	Thr	Asp	Asp	Met	195	200	205	
Ile	Gly	Ser	Met													210			

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 4285 base pairs  
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

TTTAATCTGT GTCTCCAGCA TTTATTTTTT TGTTTGTGTC ATCGGGTTCC TGGTTTTCTT	60
TTAAGACATA GTCAACTGTG TGGACCTGTA GGT TTGGGGC AGCAACCAAT TCCATTGTTT	120
TCCTTTTTGT CAAATCCAAG AGAAAATATA CCATAAGGAG CTAGAAGATT CTAGTTCACA	180
GCCTTTTGAA TCTTCATGGC CTTTGAATCC TCATGGCCTC TGAAATCTGA ATCAGTTTTTC	240
TCCCAGGARG TCTCTGGGGG CTGAGCTGCT ACAGGGG CAR ARGGTGGGGT GGGGTGGGT	300
GGGARAATCA TCCTGGCACT TCATCGTGCA TGCTATTTTCG GGCAGCATCT TTTTTTTTTT	360
ATTTTATTAT TATTTTTTTT CCTGATGCTT GAGTTATGAA TGAGGATGAC CTCTGCAATC	420
ATGATGTCTC CCATAGACTC TGTTCTTGT TCCTTTGCCA GCTTTCTCAT GCATGGTCTT	480
AACACTTCCA TGATTTAATC TGCTGCAGGA CCATAGTCTT CAGCCACCTC AGCAATAACT	540
TGTTAGAACA TTAAAAGGAA GTAAATTGAG AACAACTTGT TGCCATCCCA TTTTCATTAG	600
AAATCAGACA TCTTAGAGAT GTCAAGAAAG CAGCTAGCAG CTAGGGGGTA TGGGGACCTG	660
TCCTGCTCAC ACTGCTGTGT GTCAGACCAG ACCTGATCCT GGAGCTCAGG ACCCTAGAGA	720
GCCCTGATCT CTGGAACCTT TGCCACGTTG TTGCTGAGGC AGCTGAAGTC CCCATCTCCC	780
ACCATAACAA TCACAAATAG ACAGTAGTGG AGCCAGCATC CCCAGGCCCC TTTTGTGTA	840
AGCAGAAAGG GAGCTGTGAG CCTTGCCCTG TTTGCAGGTG TCAAGTGCCT CTCCCTGCCT	900
GTACTTCTCC CCTTCCTCTG AGCAGAGCTT TGGTAGCTGT TGCCAATGCA AAGAAATGTA	960
AAGCAGCAAA AGAAGACAGC AGGTTCTGAC CTGAGGAGGG AAACCAAATT TATCCCACAA	1020
AGGCCCATTA ACCCCACCCC CCTCGCCTCC CACCCCAGA CTGGATCCAC TACTGGCCCCA	1080
AGAATACTGA TGAGAAACCT AGTCTGGATT GGGTCGGAAG CTGGAATTTG GTGCTCTGCA	1140
GACCAGTGCT CAAAATTGTG GTTATTTTTT AGGACTCGCC TTCAATCCAG AACATTTGCG	1200
TTTCACCTTC CTCGCCAGA TCCAGTTAAC AAGGTAGCTC ATCACTTCTT GCATCTGTTG	1260
AGTGACATGC TGGATTTTAA TTTTATTGT GGTGTACTT GGATGCAAGG AATATGTTTT	1320
GTCCTCCCA ATTTAGCGCA CCATCCTGGG AAGTGCATGT CTCAGACCAA CTCCACCTTC	1380
ACCTTCACCA CCTGTCGCAT CCTGCATCCT TCAGATGAGC TCACTCGGGT CACACCAAGC	1440
CTTAACCTCAG CCCCAACTCC AGCTTGTGGC AGCACCAGCC ACTTGAAATC CACGCCGGTG	1500

GCCACACCAT	GCACTCCACG	GAGACTGAGC	CTGGCTGAGT	CCTTCACTAA	CACCCGTGAG	1560
TCCACGACCA	CCATGAGCAC	ATCCCTGGGG	CTCGTGTGGC	TGTTGAAGGA	GCGGGGCATT	1620
TCTGCTGCCG	TGTACGACCC	CCAGAGCTGG	GACAGGGCCG	GCCGGGGCTC	CCTCCTGCAC	1680
TCCTACACGC	CCAAGATGGC	TGTGATCCCC	TCTACTCCGC	CGAACTCGCC	TATGCAGACA	1740
CCCACATCCT	CCCCACCCTC	CTTTGAGTTC	AAGTGCACGA	GCCCTCCCTA	CGACAATTTT	1800
CTGGCTTCCA	AGCCAGCCAG	CTCCATCCTG	AGGGAAGTGA	GAGAAAAGAA	CGTCCGCAGC	1860
AGCGAGAGCC	AGACCGACGT	GTCCGTCTCC	AACCTCAACC	TCGTGGACAA	AGTCAGGAGG	1920
TTTGGGGTGG	CCAAAGTGGT	GAACTCAGGG	CGAGCCCATG	TCCCCACCTT	GACTGAGGAG	1980
CAGGGACCCC	TCCTCTGTGG	GCCCCCGGGG	CCAGCACCAG	CCCTTGTTCC	CAGAGGCCTG	2040
GTACCTGAGG	GCCTGCCCCT	CAGATGCCCC	ACTGTCACCA	GTGCCATCGG	TGGGCTGCAG	2100
CTCAATAGTG	GCATCCGGCG	GAATCGCAGC	TTCCCCACCA	TGGTGGGATC	TAGCATGCAG	2160
ATGAAAGCTC	CTGTGACTCT	CACCTCGGGC	ATCTTGATGG	GTGCTAAGCT	CTCCAAACAA	2220
ACTAGCTTAC	GGTGAGGACT	GGAGGGGGGC	CGGTTGCCCT	AGAGGAGACC	CACGTTCTCT	2280
CTTGCTCCCA	CCTCCCTCTC	TTCCCCCCAC	AGTGCCTCC	CTCCCTCTGC	CCTTCTCTGT	2340
CCACCCCTC	CTAAGCTAGA	CAAATCAACC	TTGTGCCTAA	TGGAGGAAGT	GTGGAAACTT	2400
TGTAAAATGT	GTACATAGGA	CTTGGAGACC	TTGTGTCCGC	CCTGCTCTTT	CTTCCGATCC	2460
CACAGGAAGT	GCCCCTGCAC	TGTCATCACT	CTCACGAGGA	CGTCACCTGT	GCTAACCTGG	2520
GGGAAGGTGG	GGTCCTTTCT	TCTTTCCTTT	TGAGAAGCAC	TGAAACTCCC	AAGTGTGTTC	2580
TTATCCCATG	GATAGGAAAC	CAGTGAATTC	CGTGGCTGGC	ACACCACGAG	CTGTCATGCG	2640
GCACGGGTCA	TAACACATCT	GGGTGTCATC	GGACACCTCA	CCTCGCCAC	CCTGTAGGAG	2700
CGTAAGGAGC	CTCCATCCTC	AGCCACGTGC	AGCTGACGTG	GCTTTCCTGA	TCGGAGGGCT	2760
TTTCTTTTAT	GGGTGGCCCA	GCTTCTTCAA	GACCTTCACT	GCTCTGCCTC	AGTGGACAGT	2820
CGTTTCTTTT	TTGAGGTGTG	ACCTTTTGTT	TTCATGCCTT	CCCCTGAAG	TCATCCTGTG	2880
TTTTGTAAATC	AGCTGTCAGG	CCAAATGTCT	GACCCGAAAG	AGAATGTATT	TAACTCATG	2940
CTGCGTTGTT	CAGCAGCCCC	TCTGTGTTCT	GTGTGATTTG	TTTTATTTTT	CCTTTTTTTT	3000
ACATATATAT	GCAGGGAAGT	AATGGTACTG	GTAGTGTATG	TTTTCTATGT	GGTTCAAATA	3060
TGAATTTTCGA	ACACACCAAG	CCGCTAATGA	GATAGCAGCT	TTTTTCTGGG	ACCCAGAGTC	3120
ACAACCAAAT	TGATTTAAGA	CCGGACCCAA	GACACCTTTA	ACAATAGGAC	TGAAAGGAAA	3180
AAGGATAGGG	AAAAAGCTTA	TTAAAGAAAT	GTGTCAACAC	CAAATGTAGA	GGGGAAGAAC	3240

CACAACCAGG CATAATACCA AACCGGTTCC AGGGGGAAAC AAGGCTTTGG TATTCCGCTG	3300
GCTCCAGCGC TTTTCTGAA ACCCGAGGCT GGCCAGGGTG CTGTCACCGT GTGGTCTTTG	3360
ATTGCAGCCA TTCAATGCCC ACATGCTTTT CCTTCTTGTT TCAGAACAGC ACATGGTCAC	3420
AACAAGATAT TTTCTTTCCC TCCAAAGCCT TTTGTCTCCT TGTGCCTCTT TTTATCCTTA	3480
GGAAAAGATC CAGGTGCTTG TGAAAAGAAT CATGAATGCA ACAAGGGAGG CTGGTCCTGT	3540
TGCTGTCGCC GATTAAGTTT TAAACTTTTA TTTATTATTT ATGTCTGCCG TATTTTAAAT	3600
AAACATTCTC GTTCCTTCCA GTTCCAGTCA TAGTGTGTCT GTGGCATTCC AGTCCAACCA	3660
TGTGACTTAT TTATTCTAAT TTGAGGGCTG CACTGTACAC CATGGTGTCC TGTGACACCG	3720
TGTTCCAGAC ATTTATGGAA GGAAAACATC CCATATAAAT GAAACTGTCA TGCTGTGTCC	3780
TCCCCGGCAG CAGAAGATGT GTCCTTCCAT TGAGTGAGGG TAACCTTATG TCCACCAAGG	3840
ATACTTTGAG AAAGCCCCTA AGGAACAAGC CTCAGTCCCA CGGTTTCAGA CTATTTATTC	3900
TCTGAACACA AGAGTATTGG TTAATTATGT TCTCAGCTCT CCCTGCTGTT GTATGTGTGC	3960
ATTCACTGCA AGTAACTTAT ATCTTTTTAT TTGAATGTAT TT'FAAGCAG TAGATAGAAT	4020
AACAAAGGAA TATGAAAACC ATGGACTGAA TGGACCATTT TATGTATTCA GAGAGAGAAG	4080
CCACTCATCA TTGCCAGAAA TACCATGTAA AAATTGGCAG TTCAGAGGTT GCAATACTTA	4140
GTATAGTAAA TAAATAAACG GTCAACATTG TGCAACCACT ACCAAAAAGT GTGTTGTAAT	4200
GCATCAAAAA TCAACACAAT TTTATTCACT AATGAGTATC AATAAAATAA GTTCAAATGA	4260
TGGAAACCAC AAAAAAAAAA AAAAA	4285

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 429 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

Met	Gln	Arg	Asn	Val	Lys	Gln	Gln	Lys	Lys	Thr	Ala	Gly	Ser	Asp	Leu
1				5				10						15	
Arg	Arg	Glu	Thr	Lys	Phe	Ile	Pro	Gln	Arg	Pro	Ile	Asn	Pro	Thr	Pro
			20					25					30		
Leu	Ala	Ser	His	Pro	Gln	Thr	Gly	Ser	Thr	Thr	Gly	Pro	Arg	Ile	Leu

35					40					45					
Met	Arg	Asn	Leu	Val	Trp	Ile	Gly	Ser	Glu	Ala	Gly	Ile	Trp	Cys	Ser
50						55					60				
Ala	Asp	Gln	Cys	Ser	Lys	Leu	Trp	Leu	Phe	Leu	Arg	Thr	Arg	Leu	Gln
65					70					75					80
Ser	Arg	Thr	Phe	Ala	Phe	His	Leu	Pro	Arg	Pro	Asp	Pro	Val	Asn	Lys
				85					90					95	
Val	Ala	His	His	Phe	Leu	His	Leu	Leu	Ser	Asp	Met	Leu	Asp	Phe	Asn
			100					105					110		
Phe	Tyr	Cys	Gly	Cys	Thr	Trp	Met	Gln	Gly	Ile	Cys	Phe	Val	Pro	Pro
	115						120					125			
Asn	Leu	Ala	His	His	Pro	Gly	Lys	Cys	Met	Ser	Gln	Thr	Asn	Ser	Thr
	130					135					140				
Phe	Thr	Phe	Thr	Thr	Cys	Arg	Ile	Leu	His	Pro	Ser	Asp	Glu	Leu	Thr
145					150					155					160
Arg	Val	Thr	Pro	Ser	Leu	Asn	Ser	Ala	Pro	Thr	Pro	Ala	Cys	Gly	Ser
				165					170					175	
Thr	Ser	His	Leu	Lys	Ser	Thr	Pro	Val	Ala	Thr	Pro	Cys	Thr	Pro	Arg
			180					185					190		
Arg	Leu	Ser	Leu	Ala	Glu	Ser	Phe	Thr	Asn	Thr	Arg	Glu	Ser	Thr	Thr
	195						200					205			
Thr	Met	Ser	Thr	Ser	Leu	Gly	Leu	Val	Trp	Leu	Leu	Lys	Glu	Arg	Gly
	210					215					220				
Ile	Ser	Ala	Ala	Val	Tyr	Asp	Pro	Gln	Ser	Trp	Asp	Arg	Ala	Gly	Arg
225					230					235					240
Gly	Ser	Leu	Leu	His	Ser	Tyr	Thr	Pro	Lys	Met	Ala	Val	Ile	Pro	Ser
				245					250					255	
Thr	Pro	Pro	Asn	Ser	Pro	Met	Gln	Thr	Pro	Thr	Ser	Ser	Pro	Pro	Ser
			260				265						270		
Phe	Glu	Phe	Lys	Cys	Thr	Ser	Pro	Pro	Tyr	Asp	Asn	Phe	Leu	Ala	Ser
	275						280					285			
Lys	Pro	Ala	Ser	Ser	Ile	Leu	Arg	Glu	Val	Arg	Glu	Lys	Asn	Val	Arg
	290					295					300				
Ser	Ser	Glu	Ser	Gln	Thr	Asp	Val	Ser	Val	Ser	Asn	Leu	Asn	Leu	Val
305					310					315					320
Asp	Lys	Val	Arg	Arg	Phe	Gly	Val	Ala	Lys	Val	Val	Asn	Ser	Gly	Arg
				325					330					335	
Ala	His	Val	Pro	Thr	Leu	Thr	Glu	Glu	Gln	Gly	Pro	Leu	Leu	Cys	Gly

340	345	350
Pro Pro Gly Pro Ala Pro Ala Leu Val Pro Arg Gly Leu Val Pro Glu		
355	360	365
Gly Leu Pro Leu Arg Cys Pro Thr Val Thr Ser Ala Ile Gly Gly Leu		
370	375	380
Gln Leu Asn Ser Gly Ile Arg Arg Asn Arg Ser Phe Pro Thr Met Val		
385	390	395
Gly Ser Ser Met Gln Met Lys Ala Pro Val Thr Leu Thr Ser Gly Ile		
405	410	415
Leu Met Gly Ala Lys Leu Ser Lys Gln Thr Ser Leu Arg		
420	425	

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3751 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

ACTTTGAATT TTTTATTTGT GAAATTAAAA ATATGGTATT ATATATATAT AAACCTTCTAT	60
TCCTCTATAA ATATAGATGA TTTTGTGATA GTGAACAGAA TAAATGTATA CCAAATTCAA	120
AGACCAATAT CATTTTAGCG TATGACAGAC ATAGATAAAT TTAGGTCCTA AGTACCGGCA	180
TTTTGATAAA TTCTTAAAGT TTAACAACAT ACAATCAGGA GGATTGCTTT TCTCCTCTTC	240
TTCACAGAGA ACTAAAGTGA ATATTTTTAA ATGGCTTTGA AAGATTTACA TTTGACACAT	300
TTCTGTAAAT CCAAAGAGG AGCACACAGG GATTTAATGC AGTAGACCTG CACACATTTT	360
CCCTTTAGCA TGCATGCCCA TATTTTGTTT ATTTTCAGGCG CTATCTCCCC GTCAATTATT	420
CCACCTTCTT TACCTCCTGA AATCTTACCA GGTTATTATT GGTGGTGTGA ATTGTTCCCC	480
CCTCAGAATG TGCTGCTGAA TAATAATCGT AATAAAATGT TGAAAGTGTA CAACTTTTAC	540
ATTTTAAAGT TTCTGATATA TGTCTAGTTA TTTGATTAAA AATAAGAAAA TAGCACTTCA	600
TTTTGAGGAA GTCCATGACA CTGAAATATC CTTCAAGTTT TCAATTTCTG TTTACGTTTT	660
GCTGTCTTGT TAAGGAAAGC AAACATCAAC TCCTTAACAA AGCTTTCCAG GTGACCTCAA	720
CATTTCCATT TTACAGACCG GTAAAATCTA AGCGCAGGCT GTCTCATTCT CAAAGGCAAG	780
GTTGCCAGGC ATCCGTATGC AATTAGAATT AACATTTTAT AACCCATATC TTCAGTCTCT	840



TCCAACCCAC	ACAAAGCTTC	ATGCTTCTTC	CCAAATCTCA	GTAACCACAT	CTTTCCATGA	900
CGCTGGCCAA	ACCCATACCA	GGTTTTAGAC	ACTAGAGAAT	GAAATGAGCT	CACCCCTCAA	960
AAATTAGACT	TCAAAAAGTT	TGGCATTGGT	TATCTCACTC	ACCCTGTAAC	CAACTAAGGT	1020
GGGAGAAGGG	AGTGTCTGGC	GTTGAAGGTG	ACCGTGGAGG	GAGGCTGAGA	CTGCCAGCGC	1080
CCACACCCGT	GGGCCCCCAT	GAAGTTGGAG	GAAAGTTCTG	GACAGTTAAA	AATCCAGCTT	1140
CAGGAAGTCG	AAGGGACGGG	CCTTCGCAAT	CCACCGCCGA	GCAAGGGAGG	AATTGTAATG	1200
TATGGGGGCC	CTCCTCCAGA	TTTGGAAGGT	TTGTGGAGTT	CTGTACCTTA	AGAGCCCCTA	1260
CCTCAAGCCA	GGAAAGAAAG	GGAGGGGACA	GAAGGAGGGG	GAGGGGGCAA	AAGGAGGAGG	1320
CGGGAAGTGA	CCCTGGCAGC	GCAGCCCTAG	TCGCACCCCG	CAGTGCTGAA	CTCGCCCCGG	1380
AGCTGGCGCC	CAGCCGTCCC	GAGCACCCGT	GGTAGGGAGA	GGCGCGCGAG	GACGACCAGG	1440
AGCGCTGTGC	GGTTGCACAC	CAGTTTTAGC	TCCTTTGCAA	TACTCCGAAA	AGGGCAAGAA	1500
GAAAAGCCTC	AAATGGTTAA	ACCGCCCTAA	ATAATTAAAA	ACTTTTGAAA	AAGAAAAACG	1560
CGTGATCGGT	CGTCATTTAA	ATACAAATAT	ACTTACAAAA	ATCCTACACA	GGCTATTTAC	1620
AATCATAAAA	GCGAACAGTC	CTGGTACCAG	AGTGTGAGGG	CAAGAGGTCT	GTCCATCCTC	1680
CCTCTGGCAG	TCGGGCCCTC	GTGTCCTTTT	GCCTCAGGGA	CGGAAGCTTT	TGCAGGAGCT	1740
GAGTTGTTCT	AGGCCTCTTT	GGCCGAATTC	GGCCAAAGAG	GCCTAATTCC	TTCCTCGGTT	1800
ATTTCAATTCA	GAGAATATTT	ATGAAATGCC	TACTGTGTGC	AAGTCATCCA	TCCTTGAAAA	1860
GGCCACTTCT	CAGTGAGGGA	GAGATGTAGT	GGATTCTGTG	AGACATACCT	GCTGGAGTTG	1920
AAGCAGTAAA	TAGCATGTCT	TCCCCCTCCC	CGATCTTAAG	GTGTGTTTTT	TAGAAAAGTT	1980
CCCTAATGGA	ATTCATGAGT	TTGGGGGTCT	CAGTCACCCG	CTTGCCTGTA	GGATTCCATT	2040
TGATGATTCT	GGATTTTTGC	TGTTTGTTAT	TGCCCTTAGA	GGGGCTCTGA	GTATCTACTT	2100
GTGGGTGGCC	ATTCCTGAC	ATCTGCATGT	ACCTCGTGGA	ATTCAGCCAG	CTTCATGTTG	2160
CAAATCAGAA	AGCTGACCCC	AAGACTGCAA	ATCAATGAAG	GTATTGGCAT	TGTTAAGGTC	2220
GTAGCGTAGA	CAACAGCAGT	CATAAATAAT	TAGGCAGGAA	CTTAACCCAA	ATCTAGTTCT	2280
TTGACCACCT	CTACCACCAG	AACCCAGCAG	ACACTCACAT	CTCCTGATAA	GAGTTGCTGG	2340
ACTCGATGTT	TTTGTTTTGC	ATTTTCTCCT	CTCCTTCCCC	ACTTACTCAG	AGAATTTAAA	2400
GTCTGTAGAG	TCAGCACAGC	CCCATCAGTC	CAGGAACTTC	CCACCACCAG	CCCTTGACTG	2460
TCCCATTAAAC	TGACATGGTC	AGATTTCCAG	CTCCCCCTAC	TCCCTGCTGT	GAAACAATCC	2520

CTCTCCYTGT GAGAGGAAAY TGC GCGSGAA GGYTAAGGGA GTGTGGCGGG CGGYTCCGGG	2580
AGCCAACATG CCTCGGTATG CGCAGCTGKT CATGGSCCCC GCGGGCAGCG GGAAGAGCAC	2640
YTACTGTGCC ACCATGGTCC AGCACTGTGA AGCCYTCAAC CGGTCTGTCC AAGTTGTAAA	2700
CCTGGATCCA GCAGCAGAAC ACTTCAAYTA CTCCGTGATG GCTGACATCC GGGAACTGAT	2760
CGAGGTGGAT GATGTAATGG AGGATGATTY TYTGCGATTG GGTCCCAACG GAGGATTGGT	2820
ATTTTGCATG GAGTACTTTG CCAATAATTT TGACTGGCTG GAGAACTGTC TTGGCCATGT	2880
AGAGGACGAC TATATCCTTT TTGATTGTCC AGGTCAGATT GAGTTGTACA CTCACCTGCC	2940
TGTGATGAAA CAGCTGGTCC AGCAGCTCGA GCAGTGGGAG TTCCGAGTCT GTGGAKTTTY	3000
TYTTGTTGAT TCTCAGTTCA TGGTGGAGTC ATTCAAGTTT ATTTCTGGCA TCTTGGCAGC	3060
CCTGAGTGCC ATGATCTCTC TAGAAATTCC GCAAGTCAAC ATCATGACAA AAATGGATCT	3120
GCTGAGTAAA AAAGCAAAAA AGGAAATTGA GAAATTTTTA GATCCAGACA TGTATTCTTT	3180
ATTAGAAGAT TCTACAAGTG ACTTAAGAAG CAAAAAATTC AAGAACTGA CTAAAGCTAT	3240
ATGTGGACTG ATTGATGACT ACAGCATGGT TCGATTTTTA CCTTACGATC AGTCAGATGA	3300
AGAAAGCATG AACATTGTAT TGCAGCATAT TGATTTTGCC ATTCAATATG GAGAAGACCT	3360
AGAATTTAAA GAACCAAAGG AACGTGAAGA TGAGTCTTCC TCTATGTTTG ACGAATATTT	3420
TCAAGAATGC CAGGATGAAT GAAGAGTTTA CTAAAAGTAA CCATCTAAAG AGCTTGTGGC	3480
CAAACCAGCA GAACATTCTT CTYTTCAAAG GATGCAATAG TAGAAAGCTA CTTATTTTAA	3540
TGAAAAAAG TAAAACTTCG TTCTTTATCA GCCTCATGCC TGAATCAAAT TTTTAATTAT	3600
TCTGAAACTG CTGCTGTTTA AAGTGGAAATC TTTTAGTATT ATAACAGCAT CACTTTAGAT	3660
TTTGTAAGTC AAAATTGAAA TGAATGCACA TAGATTTATA TATAAATTAG CACCTGAGCT	3720
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA A	3751

(2) INFORMATION FOR SEQ ID NO:207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

Met Pro Arg Tyr Ala Gln Leu Xaa Met Xaa Pro Ala Gly Ser Gly Lys

1	5	10	15
Ser Thr Tyr Cys Ala Thr Met Val Gln His Cys Glu Ala Xaa Asn Arg	20	25	30
Ser Val Gln Val Val Asn Leu Asp Pro Ala Ala Glu His Phe Asn Tyr	35	40	45
Ser Val Met Ala Asp Ile Arg Glu Leu Ile Glu Val Asp Asp Val Met	50	55	60
Glu Asp Asp Xaa Leu Arg Phe Gly Pro Asn Gly Gly Leu Val Phe Cys	65	70	75
Met Glu Tyr Phe Ala Asn Asn Phe Asp Trp Leu Glu Asn Cys Leu Gly	85	90	95
His Val Glu Asp Asp Tyr Ile Leu Phe Asp Cys Pro Gly Gln Ile Glu	100	105	110
Leu Tyr Thr His Leu Pro Val Met Lys Gln Leu Val Gln Gln Leu Glu	115	120	125
Gln Trp Glu Phe Arg Val Cys Gly Xaa Xaa Xaa Val Asp Ser Gln Phe	130	135	140
Met Val Glu Ser Phe Lys Phe Ile Ser Gly Ile Leu Ala Ala Leu Ser	145	150	155
Ala Met Ile Ser Leu Glu Ile Pro Gln Val Asn Ile Met Thr Lys Met	165	170	175
Asp Leu Leu Ser Lys Lys Ala Lys Lys Glu Ile Glu Lys Phe Leu Asp	180	185	190
Pro Asp Met Tyr Ser Leu Leu Glu Asp Ser Thr Ser Asp Leu Arg Ser	195	200	205
Lys Lys Phe Lys Lys Leu Thr Lys Ala Ile Cys Gly Leu Ile Asp Asp	210	215	220
Tyr Ser Met Val Arg Phe Leu Pro Tyr Asp Gln Ser Asp Glu Glu Ser	225	230	235
Met Asn Ile Val Leu Gln His Ile Asp Phe Ala Ile Gln Tyr Gly Glu	245	250	255
Asp Leu Glu Phe Lys Glu Pro Lys Glu Arg Glu Asp Glu Ser Ser Ser	260	265	270
Met Phe Asp Glu Tyr Phe Gln Glu Cys Gln Asp Glu	275	280	

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

TNCAGGCCTT GCGTTCCTAG CTGCTCTGC

29

(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

GNGCTGTGAG TTTATCCACA AAGGAACAG

29

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

GNATAGGAGG TCCCAAGTTA TCAAGGTTT

29

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:  
GNTTTCCTGG TTCTTGGTCA GGTTTCCTC 29

(2) INFORMATION FOR SEQ ID NO:212:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 29 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid  
    (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:  
CNAGATGCAA TGGTTGTGAG ATTGACCAA 29

(2) INFORMATION FOR SEQ ID NO:213:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 29 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid  
    (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:  
GNCACTTTCC ACTGCTGTGA GCTTGTCAT 29

(2) INFORMATION FOR SEQ ID NO:214:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 29 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid  
    (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:  
ANCAGACAGT TTGCCATGGA GTACATCAC 29

(2) INFORMATION FOR SEQ ID NO:215:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

TNATGAACCA CAGGAAACAG GAAGCCGTC

29

(2) INFORMATION FOR SEQ ID NO:216:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

TNAAGGTGAA GGTGGAGTTG GTCTGAGAC

29

(2) INFORMATION FOR SEQ ID NO:217:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

GNCAGAAATA AACTTGAATG ACTCCACCA

29

(2) INFORMATION FOR SEQ ID NO:218:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 457 amino acids
  - (B) TYPE: amino acid

(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

Met Asn Ser Gln Leu Asn Ser Phe Thr Gly Gln Met Glu Asn Ile Thr  
1 5 10 15  
Thr Ile Ser Gln Ala Asn Glu Gln Asn Leu Lys Asp Leu Gln Asp Leu  
20 25 30  
His Lys Asp Ala Glu Asn Arg Thr Ala Ile Lys Phe Asn Gln Leu Glu  
35 40 45  
Glu Arg Phe Gln Leu Phe Glu Thr Asp Ile Val Asn Ile Ile Ser Asn  
50 55 60  
Ile Ser Tyr Thr Ala His His Leu Arg Thr Leu Thr Ser Asn Leu Asn  
65 70 75 80  
Glu Val Arg Thr Thr Cys Thr Asp Thr Leu Thr Lys His Thr Asp Asp  
85 90 95  
Leu Thr Ser Leu Asn Asn Thr Leu Ala Asn Ile Arg Leu Asp Ser Val  
100 105 110  
Ser Leu Arg Met Gln Gln Asp Leu Met Arg Ser Arg Leu Asp Thr Glu  
115 120 125  
Val Ala Asn Leu Ser Val Ile Met Glu Glu Met Lys Leu Val Asp Ser  
130 135 140  
Lys His Gly Gln Leu Ile Lys Asn Phe Thr Ile Leu Gln Gly Pro Pro  
145 150 155 160  
Gly Pro Arg Gly Pro Arg Gly Asp Arg Gly Ser Gln Gly Pro Pro Gly  
165 170 175  
Pro Thr Gly Asn Lys Gly Gln Lys Gly Glu Lys Gly Glu Pro Gly Pro  
180 185 190  
Pro Gly Pro Ala Gly Glu Arg Gly Pro Ile Gly Pro Ala Gly Pro Pro  
195 200 205  
Gly Glu Arg Gly Gly Lys Gly Ser Lys Gly Ser Gln Gly Pro Lys Gly  
210 215 220  
Ser Arg Gly Ser Pro Gly Lys Pro Gly Pro Gln Gly Pro Ser Gly Asp  
225 230 235 240  
Pro Gly Pro Pro Gly Pro Pro Gly Lys Glu Gly Leu Pro Gly Pro Gln  
245 250 255  
Gly Pro Pro Gly Phe Gln Gly Leu Gln Gly Thr Val Gly Glu Pro Gly  
260 265 270

Val Pro Gly Pro Arg Gly Leu Pro Gly Leu Pro Gly Val Pro Gly Met  
 275 280 285  
 Pro Gly Pro Lys Gly Pro Pro Gly Pro Pro Gly Pro Ser Gly Ala Val  
 290 295 300  
 Val Pro Leu Ala Leu Gln Asn Glu Pro Thr Pro Ala Pro Glu Asp Asn  
 305 310 315 320  
 Ser Cys Pro Pro His Trp Lys Asn Phe Thr Asp Lys Cys Tyr Tyr Phe  
 325 330 335  
 Ser Val Glu Lys Glu Ile Phe Glu Asp Ala Lys Leu Phe Cys Glu Asp  
 340 345 350  
 Lys Ser Ser His Leu Val Phe Ile Asn Thr Arg Glu Glu Gln Gln Trp  
 355 360 365  
 Ile Lys Lys Gln Met Val Gly Arg Glu Ser His Trp Ile Gly Leu Thr  
 370 375 380  
 Asp Ser Glu Arg Glu Asn Glu Trp Lys Trp Leu Asp Gly Thr Ser Pro  
 385 390 395 400  
 Asp Tyr Lys Asn Trp Lys Ala Gly Gln Pro Asp Asn Trp Gly His Gly  
 405 410 415  
 His Gly Pro Gly Glu Asp Cys Ala Gly Leu Ile Tyr Ala Gly Gln Trp  
 420 425 430  
 Asn Asp Phe Gln Cys Glu Asp Val Asn Asn Phe Ile Cys Glu Lys Asp  
 435 440 445  
 Arg Glu Thr Val Leu Ser Ser Ala Leu  
 450 455

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 542 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

Cys Gly His His Glu Leu Asn Asn Leu Asn Leu Thr Gln Val Gln Gln  
 1 5 10 15  
 Arg Asn Leu Ile Thr Asn Leu Gln Arg Ser Val Asp Asp Thr Ser Gln  
 20 25 30



Ala	Ile	Gln	Arg	Ile	Lys	Asn	Asp	Phe	Gln	Asn	Leu	Gln	Gln	Val	Phe	35	40	45	
Leu	Gln	Ala	Lys	Lys	Asp	Thr	Asp	Trp	Leu	Lys	Glu	Lys	Val	Gln	Ser	50	55	60	
Leu	Gln	Thr	Leu	Ala	Ala	Asn	Asn	Ser	Ala	Leu	Ala	Lys	Ala	Asn	Asn	65	70	75	80
Asp	Thr	Leu	Glu	Asp	Met	Asn	Ser	Gln	Leu	Asn	Ser	Phe	Thr	Gly	Gln	85	90	95	
Met	Glu	Asn	Ile	Thr	Thr	Ile	Ser	Gln	Ala	Asn	Glu	Gln	Asn	Leu	Lys	100	105	110	
Asp	Leu	Gln	Asp	Leu	His	Lys	Asp	Ala	Glu	Asn	Arg	Thr	Ala	Ile	Lys	115	120	125	
Phe	Asn	Gln	Leu	Glu	Glu	Arg	Phe	Gln	Leu	Phe	Glu	Thr	Asp	Ile	Val	130	135	140	
Asn	Ile	Ile	Ser	Asn	Ile	Ser	Tyr	Thr	Ala	His	His	Leu	Arg	Thr	Leu	145	150	155	160
Thr	Ser	Asn	Leu	Asn	Glu	Val	Arg	Thr	Thr	Cys	Thr	Asp	Thr	Leu	Thr	165	170	175	
Lys	His	Thr	Asp	Asp	Leu	Thr	Ser	Leu	Asn	Asn	Thr	Leu	Ala	Asn	Ile	180	185	190	
Arg	Leu	Asp	Ser	Val	Ser	Leu	Arg	Met	Gln	Gln	Asp	Leu	Met	Arg	Ser	195	200	205	
Arg	Leu	Asp	Thr	Glu	Val	Ala	Asn	Leu	Ser	Val	Ile	Met	Glu	Glu	Met	210	215	220	
Lys	Leu	Val	Asp	Ser	Lys	His	Gly	Gln	Leu	Ile	Lys	Asn	Phe	Thr	Ile	225	230	235	240
Leu	Gln	Gly	Pro	Pro	Gly	Pro	Arg	Gly	Pro	Arg	Gly	Asp	Arg	Gly	Ser	245	250	255	
Gln	Gly	Pro	Pro	Gly	Pro	Thr	Gly	Asn	Lys	Gly	Gln	Lys	Gly	Glu	Lys	260	265	270	
Gly	Glu	Pro	Gly	Pro	Pro	Gly	Pro	Ala	Gly	Glu	Arg	Gly	Pro	Ile	Gly	275	280	285	
Pro	Ala	Gly	Pro	Pro	Gly	Glu	Arg	Gly	Gly	Lys	Gly	Ser	Lys	Gly	Ser	290	295	300	
Gln	Gly	Pro	Lys	Gly	Ser	Arg	Gly	Ser	Pro	Gly	Lys	Pro	Gly	Pro	Gln	305	310	315	320
Gly	Pro	Ser	Gly	Asp	Pro	Gly	Pro	Pro	Gly	Pro	Pro	Gly	Lys	Glu	Gly	325	330	335	

Leu Pro Gly Pro Gln Gly Pro Pro Gly Phe Gln Gly Leu Gln Gly Thr  
 340 345 350

Val Gly Glu Pro Gly Val Pro Gly Pro Arg Gly Leu Pro Gly Leu Pro  
 355 360 365

Gly Val Pro Gly Met Pro Gly Pro Lys Gly Pro Pro Gly Pro Pro Gly  
 370 375 380

Pro Ser Gly Ala Val Val Pro Leu Ala Leu Gln Asn Glu Pro Thr Pro  
 385 390 395 400

Ala Pro Glu Asp Asn Ser Cys Pro Pro His Trp Lys Asn Phe Thr Asp  
 405 410 415

Lys Cys Tyr Tyr Phe Ser Val Glu Lys Glu Ile Phe Glu Asp Ala Lys  
 420 425 430

Leu Phe Cys Glu Asp Lys Ser Ser His Leu Val Phe Ile Asn Thr Arg  
 435 440 445

Glu Glu Gln Gln Trp Ile Lys Lys Gln Met Val Gly Arg Glu Ser His  
 450 455 460

Trp Ile Gly Leu Thr Asp Ser Glu Arg Glu Asn Glu Trp Lys Trp Leu  
 465 470 475 480

Asp Gly Thr Ser Pro Asp Tyr Lys Asn Trp Lys Ala Gly Gln Pro Asp  
 485 490 495

Asn Trp Gly His Gly His Gly Pro Gly Glu Asp Cys Ala Gly Leu Ile  
 500 505 510

Tyr Ala Gly Gln Trp Asn Asp Phe Gln Cys Glu Asp Val Asn Asn Phe  
 515 520 525

Ile Cys Glu Lys Asp Arg Glu Thr Val Leu Ser Ser Ala Leu  
 530 535 540